

# FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA  
CCCACCGCGTCCGGGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCG  
CAGCGCTACCCGCCATGCGCCTGCCGCCGGCGCGCTGGGGCTCCTGCCGCTTCTGCTG  
CTGCTGCCGCCGCCGGAGGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCT  
GGTGGACAAGTTAACCAAGGGATGGTGACACCGCAAAGAAGAACTTGGCGGGGGAAACA  
CGGCTTGGGAGGAAAAGACGCTGTCAAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC  
CTGGAGGGCTGTGCAGAGCAGCAGTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA  
GCACCTGGAGGCCTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT  
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCAGTGTCTCGCATGC  
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGGAGATGGGAGCAGACA  
GGCGACGGGTCTGCCGTGCCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG  
ACGGCTACTTCAGCTCGCTCCGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC  
TGCAAGACGTGCTCGGCCTGACCAACAGAGACTGCGGCAGTGTGAAGTGGCTGGTGCT  
GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTG  
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG  
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCAGGGAGCA  
CGGACAGTGTGCAGATGTGGACGAGTGTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACG  
AAAATGCTACAATACTCCAGGGAGCTACGTCTGTGTGCTGACGGCTTCGAAGAACG  
GAAGATGCCTGTGTGCCGCCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT  
GCCCTCCCGCAAGACCTGTAATGTGCCGGACTTACCCTTAAATTATTAGAAGGATGTCC  
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGGGGAGAGGCTGC  
CTGCTCTCTAACGGTGATTCTCATTGTCCTTAAACAGCTGCATTCTGGTTGTTCTTA  
AACAGACTTGTATATTTGATACAGTTCTTGTAATAAAATTGACCATTGTAGGTAATCAGG  
AGGAAAAAAAGGGCGCCGCGACTCTAGAGTCGACCTGCAGAACG  
TTGGCCGCCATGGCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAGCAATAGCA  
TCACAAATTCAAAATAAGCATTTCAGCTAGTTGTGGTTGTCCAAACTC  
ATCAATGTATCTTATCATGTCGGATCGGAATTAAATTGCGCGCAGCACCATGGCCTGAAAT  
AACCTCTGAAAGAGGAACTTGGTTAGGTACCTCTGAGGCGGAAAGAACCCAGCTGTGGAATG  
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC  
ATCTCAATTAGTCAGCAACCCAGTTT

## **FIGURE 2**

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLPLLLLPPAPEAAKKPTPCHRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL  
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLVCCSPGTYGPDCLACQGGSQRPCSG  
NGHCGSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNEHTSICTACDESCKTCSGLTNRDCGECEVGWVLDE  
GACVDVDECAAEP PCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT  
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

**Signal peptide:**

amino acids 1-24

**N-glycosylation sites.**

amino acids 190-194 and 251-255

**Glycosaminoglycan attachment sites.**

amino acids 149-153 and 155-159

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 26-30

**Casein kinase II phosphorylation sites.**

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343  
and 349-353

**Tyrosine kinase phosphorylation site.**

amino acids 303-310

**N-myristylation sites.**

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and  
313-319

**Aspartic acid and asparagine hydroxylation site.**

amino acids 308-320

**EGF-like domain cysteine pattern signature.**

amino acids 166-178

**Leucine zipper pattern.**

amino acids 94-116

## FIGURE 3

CAGGTCCAAC TGCACCTCGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTC  
GACCTCGACCCACGCGTCCGCCAGGCCGGAGGCAGCGGCCAGCGTCTAAACGGGAACA  
GCCCTGGCTGAGGGAGCTGCAGCGCAGAGTATCTGACGGGCCAGGTTGCGTAGGTGCG  
GCACGAGGAGTTTCCCGCAGCGAGGAGGTCTGAGCAGCAGCATGGCCGGAGGAGCGCCTTC  
CCTGCCGCCGCTCTGGCTCTGGAGCATCCTCTGTGCCTGCTGGACTGCGGCCGGAGGC  
CGGGCCGCCAGGAGGAGGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCA  
TAGGATTGAAGAAGATATCCTGATTGTTAGAGGGAAAATGGCACCTTTACACATGAT  
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTCAC  
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTCTGTGCCTGCGCTCCCTGGATA  
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGAAACAGTGCTCACAAGGCA  
TCAGTTGTTCAAGTTGGTTCCATGTCTGGAAAACAGGATGGGTGGCAGCATTGAAGT  
GGATGTGATTGTTATGAATTCTGAAGGCAACACATTCTCAAACACCTCAAATGCTATCT  
TCTTAAACATGTCAACAAGCTGAGTGCCCAGGCGGGTGGCAAATGGAGGCTTTGTAAT  
GAAAGACGCATCTGCGAGTGTCCCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCTTG  
TACCCCACGATGTATGAATGGTGACTTGTGACTCCTGGTTCTGCATCTGCCACCTG  
GATTCTATGGAGTGAACTGTGACAAAGCAAACCTGCTCAACCACCTGCTTAATGGAGGAGC  
TGTTCTACCCCTGGAAAATGTATTGCCCTCAGGACTAGAGGGAGAGCAGTGTGAAATCAG  
CAAATGCCACAACCTGCGAAATGGAGGTAATGCATTGGTAAAAGCAAATGTAAGTGT  
CCAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTGCGAGCCTGGCTGTTGCACAT  
GGAACCTGCCATGAACCCAAACAAATGCCATGTCAAGAAGGTTGGCATGGAAGACACTGCAA  
TAAAGGTACGAAGCAGCCTCATACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGC  
ACACGCCCTCACTTAAAGGCCAGGGAGCGGGATCCACCTGAATCCAATTACATCTGG  
TGAACCTCGACATCTGAAACGTTTAAGTTACACCAAGTTCATAGCCTTGTAAACCTTCA  
TGTGTTGAATGTTCAAATAATGTTCAATTACACTTAAGAATACTGGCCTGAATTATTAGCT  
TCATTATAAAATCACTGAGCTGATATTACTCTCCTTTAAGTTCTAAGTACGTCTGTAG  
CATGATGGTATAGATTCTTCACTGAGCTGATATTACTCTCCTTTAAGTTCTAAGTACGTCTGTAG  
TCAGGTTAAATTTCACTGAGCTGATATTACTCTCCTTTAAGTTCTAAGTACGTCTGTAG  
GTCTGGGGGCAGGGGAACATCAGAAAGGTTAAATTGGCAAAATGCGTAAGTCACAAGAAT  
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTCACTGAGGTTATTGTCAATTAGAT  
GTTTGTACATTTTAAAAATTGCTCTAATTAAACTCTCAATACAATATATTGACC  
TTACCAATTCCAGAGATTCACTGATTTAAACACAAATTACACTGTGGTAGTGGCATT  
AAACAATATAATATTCTAAACACAATGAAATTAGGAATATAATGTATGAACTTTGCAT  
TGGCTTGAAGCAATATAATTGTTAAACAAAACACAGCTTACCTAATAACATTTAT  
ACTGTTGTATGTATAAAATAAGGTGCTGCTTAGTTTTGGAAAAA  
AAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGCTTGGC  
CGCCATGGCCAAC TTGTTATTGCAGCTTATAATG

## **FIGURE 4**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKICPPGLEGEQCEISKCPQPCRNGGKIGKSCKCSKGYQGDLCSPKVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
PESNYIW
```

**Signal peptide:**

█ amino acids 1-28

█ **N-glycosylation site.**

█ amino acids 88-92, 245-249

█ **Casein kinase II phosphorylation site.**

█ amino acids 319-323

█ **Tyrosine kinase phosphorylation site.**

█ amino acids 370-378

**N-myristoylation sites.**

█ amino acids 184-190, 185-191, 189-195, 315-321

**ATP/GTP-binding site motif A (P-loop).**

█ amino acids 285-293

**EGF-like domain cysteine pattern signature.**

█ amino acids 198-210, 230-242, 262-274, 294-306, 326-338

## FIGURE 5

CGGACGGCGGGCGTCCGGCGGTGCAGAGCCAGGAGGCCAGGGCGGAGGCCAGCCTGGG  
CCCCAGCCCACACCTTCACCAGGGCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCTAC  
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCACAGGGCTGCGGGCG  
GAGCTAGCACCGGGTCTGCACCTGCAGGGCATCCGGACGCCAGGGAGGCCGGTACTGCCAGGA  
GCAGGACCTGTGCTGCCGCGGCCGTGCCACGACTGTGCCCTGCCACCTGGCGCCATCT  
GTTACTGTGACCTCTTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC  
TGCCTCGGCGTGCCACCCCTTTCCCCGATCCAAGGATGTATGCATGGAGGTGCTATCTA  
TCCAGTCTTGGGAACGTACTGGACAACGTGAACCGTGCACCTGCCAGGAGAACAGGCAGT  
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG  
GAACCACAGCGCCTCTGGGGCATGCCATGAGGGCATTGCTACCGCCTGGGACCA  
TCCGCCCACCTTCCTCGGTATGAACATGCATGAAATTTACAGTGCCTGAACCCAGGGAG  
GTGCTTCCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCAACCTGATTCATGAGCCTTTGA  
CCAAGGCAACTGTGCAGGCTCTGGGCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT  
CAATCCATTCTCTGGGACACATGACGCCCTGTCCGTGCCAGAACCTGCTGTCTTGAC  
ACCCACCAGCAGCAGGGCTGCCCGGTGGCGTCTCGATGGTGCCTGGTGGTTCTGCGTCG  
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGAGGCTGGCC  
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGCGCCAGGCCACTGCC  
CACTGCCAACAGCTATGTTAAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCT  
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA  
TGGAGGTGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGC  
CTTGGGAGGCCAGAGAGATACGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG  
AGAGGAGACGCTGCCAGATGGAGGACGCTAAAAACTGGACTGCGGCCACTCCTGGGCC  
CAGCCTGGGGCGAGAGGGCCACTTCCGCATCGTGCAGCGGTCAATGAGTGCACATCGAG  
AGCTTGTGCTGGCGTCTGGGCGCGTGGGCATGGAGGACATGGGTCATCAGTGAGGCTG  
CGGGCACCACGCCGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGGAAGAGGCCCAATG  
GGCGGTGACCCAGCCTGCCGACAGAGCCGGCGCAGGCCGGCAGGGCGCTAAT  
CCCGCGCGGGTCTCGCTGACGCAGGCCCGCTGGGAGGCCGGCAGGCAGACTGGCG  
GAGCCCCCAGACCTCCCAGTGGGAGGGCAGGGCTGGCTGGGAAGAGCACAGCTGCAG  
ATCCCAGGCCCTGGGCCCCCCACTCAAGACTACCAAAAGCCAGGACACCTCAAGTCTCCAGC  
CCCAATACCCACCCCAATCCGTATTTTTTTTTTTTAGACAGGGTCTTGCTCCG  
TTGCCCAGGTTGGAGTGCAGTGGCCATCAGGCTCACTGTAACCTCCGACTCCTGGTTCA  
AGTGACCCTCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCACACCTGGC  
TAATTTTGATTTTGTAAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTCGAACT  
CCTGGGCTCAAGCGGTCCACCTGCCTCCGCTCCAAAGTGTGGATTGCAGGCATGAGCC  
ACTGCACCCAGCCCTGTATTCTTATTCAAGATATTTTTTCACTGTTTTAAAAA  
TAAAACCAAAAGTATTGATAAAAAAA

## **FIGURE 6**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYEQDLCCRGRADDC
ALPYLGAICYCDLFCNRRTVSDCCPDFWDFCLGVPPPFPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPORLLGHDPG
```

### N-glycosylation site.

amino acids 78-82, 161-165

### Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

### **N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230, 269-275, 378-384, 442-448

### Amidation site.

amino acids 26-30, 318-322

## Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

## **FIGURE 7**

AGGCTCCTGGCCCTTTCCACAGCAAGCTNTGCNATCCGATTGTTGTCTCAAATCCA  
ATTCTCTTGGGACACATNACGCCTGTCCTTNGCCCCAGAACCTGCTGTCTGTACACCCAC  
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTTCTCGCTGCCGAGG  
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGAGGGCTGGCCCTGCGC  
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGGCAAGGCCAGGCCACTGCCACTGC  
CCCAACAGCTATGTTAATAACAATGACATCTACCAAGGTCACTCCTGTCTACCGCCTCGGCTC  
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTATGGAGG  
TGCATGAGGACTTCTCCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTGGG  
AGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAG

## **FIGURE 8**

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCAGTGCCTGCTGTGCTACT  
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG  
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG  
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT  
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCATCCTT  
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGACCCGGCAGCTATAGGCTCTGGGGGG  
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG  
GCCCAGTGGGAGCCTGTCCTGGTTCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT  
CTGCACCCCTGTCCCCCACCTGACCCCTCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA  
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCCTCTGCTGCTGTTTC  
CATGGCCCAGCATTCTCCACCCCTTAACCCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT  
CCCTGCCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTCCCCGACCCAGCA  
GGGGACAGGCACTCAGGAGGGCCCAGTAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA  
GGACAAGAGTCGACGTGAGTTCTGGAGTCTCCAGAGATGGGCCTGGAGGCCTGGAGGAA  
GGGGCCAGGCCTCACATTGTTGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT  
AATAAACACCTGTTGGATAAGCCAAAAAA

1000 200 100 50 25 12.5 6.25 3.125 1.5625 0.78125 0.390625 0.1953125 0.09765625 0.048828125 0.0244140625 0.01220703125 0.006103515625 0.0030517578125 0.00152587890625 0.000762939453125 0.0003814697265625 0.00019073486328125 0.000095367431640625 0.0000476837158203125 0.00002384185791015625 0.000011920928955078125 0.0000059604644775390625 0.00000298023223876953125 0.000001490116119384765625 0.0000007450580596923828125 0.00000037252902984619140625 0.000000186264514923095703125 0.0000000931322574615478515625 0.00000004656612873077392578125 0.000000023283064365386962890625 0.0000000116415321826934814453125 0.00000000582076609134674072265625 0.0000000029103830456733703613125 0.00000000145519152283668518065625 0.0000000007275957614183325903125 0.00000000036379788070916629515625 0.000000000181898940354583147578125 0.0000000000909494701772915737890625 0.00000000004547473508864578689453125 0.000000000022737367544322893447265625 0.00000000001136868377216144672363125 0.00000000000568434188608072336815625 0.000000000002842170943040361680828125 0.0000000000014210854715201808404140625 0.0000000000007105427357600904202078125 0.00000000000035527136788004521010390625 0.000000000000177635683940022605051953125 0.0000000000000888178419700113025259765625 0.00000000000004440892098500565126298828125 0.000000000000022204460492502825631494453125 0.0000000000000111022302462514128157472265625 0.000000000000005551115123125706407873613125 0.0000000000000027755575615628532039368078125 0.00000000000000138777878078142660196840390625 0.000000000000000693889390390713300983201953125 0.0000000000000003469446951953566504916009765625 0.00000000000000017347234759777832524580048828125 0.000000000000000086736173798889162622900244140625 0.0000000000000000433680868994445813114501220703125 0.00000000000000002168404344972229565572506110390625 0.000000000000000010842021724861147827862530551953125 0.0000000000000000054210108624305739139312515279765625 0.0000000000000000027105054312152869569656250763953125 0.00000000000000000135525271560764347832812503819765625 0.00000000000000000067762635780382173916406250190953125 0.0000000000000000003388131789019108695820312500954765625 0.00000000000000000016940658945095543499101562500477390625 0.0000000000000000000847032947254777219955078125002386765625 0.00000000000000000004235164736273886099775390625001193390625 0.000000000000000000021175823681369430498877656250005966953125 0.00000000000000000001058791184068471524943882812500029834765625 0.000000000000000000005293955920334257762474414062500014917390625 0.0000000000000000000026469779601671288812372078125000074586953125 0.0000000000000000000013234889800835644406186039062500003739228125 0.0000000000000000000006617444900417822203093019531250000186966453125 0.00000000000000000000033087224502089111015450097656250000093483215625 0.00000000000000000000016543612251044555507750048828125000004674160390625 0.00000000000000000000008271806125522277753875002441406250000023370401953125 0.000000000000000000000041359030627611388793875001193390625000011685160390625 0.00000000000000000000002067951531380569439693750005966953125000005842580390625 0.0000000000000000000000103397576569028471984787500029834765625000002931290390625 0.000000000000000000000005169878828451423594239375000149173906250000014753453125 0.00000000000000000000000258493941422571179719718750000745869531250000003729328125 0.00000000000000000000000129246970711285589859859375000023370401953125000000186966453125 0.000000000000000000000000646234853556427949299296875000009348321562500000005842580390625 0.0000000000000000000000003231174267782139746496484375000004674160390625000000023370401953125 0.0000000000000000000000001615587133891069873248242187500000149173906250000000074586953125 0.00000000000000000000000008077935669455349366241210937500000059669531250000000029834765625 0.0000000000000000000000000403896783472767468312055546875000000233704019531250000000014917390625 0.000000000000000000000000020194839173638373415522777343750000001491739062500000000074586953125 0.000000000000000000000000010097419586819186707763886718750000000596695312500000000029834765625 0.000000000000000000000000005048709793409593353891943359375000000233704019531250000000014917390625 0.0000000000000000000000000025243548967047966779459716793750000001491739062500000000074586953125 0.0000000000000000000000000012621774483523983389729858393750000000596695312500000000029834765625 0.0000000000000000000000000006310887241761991694864929196875000000233704019531250000000014917390625 0.00000000000000000000000000031554436208809958474434945968750000001491739062500000000074586953125 0.00000000000000000000000000015777218104404979237217472968750000000596695312500000000029834765625 0.00000000000000000000000000007888609052202498918608736496875000000233704019531250000000014917390625 0.0000000000000000000000000000394430452610124945930436824968750000001491739062500000000074586953125 0.0000000000000000000000000000197215226305062472965218412496875000000596695312500000000029834765625 0.0000000000000000000000000000098607613152531236482609206496875000000233704019531250000000014917390625 0.000000000000000000000000000004930380657626561824130490324968750000001491739062500000000074586953125 0.00000000000000000000000000000246519032881328091207024964968750000000596695312500000000029834765625 0.0000000000000000000000000000012325951644066404560351247496875000000023370401953125000000014917390625 0.000000000000000000000000000000616297582203320228017562374968750000000596695312500000000074586953125 0.00000000000000000000000000000030814879110166011400878118496875000000023370401953125000000014917390625 0.0000000000000000000000000000001540743955008300570043905924968750000000596695312500000000074586953125 0.0000000000000000000000000000000770371977500415028502195296496875000000023370401953125000000014917390625 0.000000000000000000000000000000038518598875002075140095781849687500000001491739062500000000074586953125 0.0000000000000000000000000000000192592994375010375700478909249687500000000596695312500000000029834765625 0.0000000000000000000000000000000096296497187505187850239454649687500000000233704019531250000000014917390625 0.00000000000000000000000000000000481482485937525939251197273249687500000000596695312500000000074586953125 0.00000000000000000000000000000000240741242968751297196559636649687500000000233704019531250000000014917390625 0.000000000000000000000000000000001203706214843756588829831832496875000000001491739062500000000074586953125 0.000000000000000000000000000000000601853107421875344444915916496875000000000596695312500000000029834765625 0.000000000000000000000000000000000300926553710937517222245798324968750000000059669531250000000014917390625 0.00000000000000000000000000000000015046327685546875861112299164968750000000002337040195312500000000074586953125 0.000000000000000000000000000000000075231638427733754305561495832496875000000001491739062500000000029834765625 0.0000000000000000000000000000000000376158192115668752152730237649687500000000059669531250000000014917390625 0.000000000000000000000000000000000018807909605783375107136511884968750000000002337040195312500000000074586953125 0.000000000000000000000000000000000009403954802951687553568255944968750000000001491739062500000000029834765625 0.00000000000000000000000000000000000470197740147583752728412777249687500000000059669531250000000014917390625 0.000000000000000000000000000000000002350988700737918751364206386496875000000000233704019531250000000074586953125 0.000000000000000000000000000000000001175494350368958756821003193249687500000000149173906250000000029834765625 0.000000000000000000000000000000000000587747175184479375340500196875000000000059669531250000000014917390625 0.000000000000000000000000000000000000293873587542239687517850098496875000000000233704019531250000000074586953125 0.000000000000000000000000000000000000146936793771119837589250298496875000000000149173906250000000029834765625 0.000000000000000000000000000000000000073468396885559918754625149249687500000000059669531250000000014917390625 0.0000000000000000000000000000000000000367341984427799587523125746496875000000000233704019531250000000074586953125 0.0000000000000000000000000000000000000183670992213899787511562531249687500000000149173906250000000029834765625 0.0000000000000000000000000000000000000091835496106949893755781257814968750000000059669531250000000014917390625 0.0000000000000000000000000000000000000045917748053474948752875625149687500000000233704019531250000000074586953125 0.00000000000000000000000000000000000000229588740267374743751437562514968750000000149173906250000000029834765625 0.00000000000000000000000000000000000000114794370133687372375718756251496875000000059669531250000000014917390625 0.00000000000000000000000000000000000000057397185066843687518756253124968750000000233704019531250000000074586953125 0.00000000000000000000000000000000000000028698592533421837593756253124968750000000149173906250000000029834765625 0.0000000000000000000000000000000000000001434929626671091875468756251496875000000059669531250000000014917390625 0.0071746481333554593752343756251496875000000233704019531250000000074586953125 0.0035873190666777237511787562514968750000000149173906250000000029834765625 0.0017936595333388618755875625312496875000000059669531250000000014917390625 0.00089682976666943093752937562514968750000000233704019531250000000074586953125 0.000448414883333715437514787562514968750000000149173906250000000029834765625 0.00022420744166685771875373756251496875000000059669531250000000014917390625 0.0001121037208334288587518756253124968750000000233704019531250000000074586953125 0.0056051860416671442875937562514968750000000149173906250000000029834765625 0.00280259302083352218754687562514968750000000059669531250000000014917390625 0.0014012965104167610875234375625149687500000000233704019531250000000074586953125 0.00070064825520833305437511787562514968750000000149173906250000000029834765625 0.0003503241276083315218753737562514968750000000059669531250000000014917390625 0.0001751620638083315187518756253124968750000000023370401953125000000074586953125 0.008758103190833151875187562514968750000000014917390625000000029834765625 0.004379051595083315187

## FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT  
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHPDPPMALSRTPTRQISSLDT  
DPPADGPSNPLCCCFHGPAGFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVSPAPSRGQALRRAQ

**Signal peptide:**

amino acids 1-47

**N-glycosylation site.**

amino acids 31-35, 74-78, 84-88

**Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

**N-myristoylation site.**

amino acids 56-60

**Amidation site.**

amino acids 70-74

## **FIGURE 10**

CCCACGCGTCCGAACCTCTCCAGCGAGGGAGCCGCCCTGCTGCCAACCTCACTCTGT  
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGGCCATGACC  
GACCAGCTGAGCAGGCGGAGATCCCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA  
CGTCAGGTCAACGGCGTCCATCTCCGCCACGCCAGGGACGGCAACAAGTTGCCAAGC  
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTCGCATCAAAGGGCTGAGAGTGAGAAG  
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCGGAAGAGCAAAGACTG  
CGTGTTCACGGAGATCGTGTGGAGAACAACTATAACGGCCTTCCAGAACGCCGGCACGAGG  
GCTGGTTCATGGCCTTCACGCGGAGGGCGGCCAGGCTTCCCGAGCCAGAAC  
CAGCGCGAGGCCCACTTCATCAAGCGCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC  
CGAGAACGAGAACAGCAGTCGAGTTGTGGCTCCGCCACCCGCCAGAAC  
GGCGGCCCAAGCCCTCACGTAGTCTGGGAGGCAGGGGCAGCAGCCCTGGCCGCTCCC  
CACCCCTTCCCTTTAATCCAAGGACTGGGCTGGGTGGCGGGAGGGGAGCCAGATCCC  
GAGGGAGGACCCCTGAGGGCCCGAAGCATCCGAGCCCCCAGCTGGGAAGGGCAGGCCGGTG  
CCCCAGGGCGGCTGGCACAGTGCCCTTCCCGACGGTGGCAGGCCCTGGAGAGGAAC  
GAGTGTCAACCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCCTGAAGCC  
CGCTGAAAGGTCAAGCGACTGAAGGCCTTGCAGACAACCGTCTGGAGGTGGCTGTCTCAAAA  
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCAGGAAACCTCTGGCTAGACTGTA  
GGAAGGGACTTTGTTGTTGTTGTTCAAGAAAAAAAGAAAGGGAGAGAGAGGAAAATAG  
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCAACTCCAGCCC  
CGGAATAAAACCATTTCCTGC

## **FIGURE 11**

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI  
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKSKDCVFTEIVLE  
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF  
VGSAPTRRTKRTRRPQPLT

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 9-13, 126-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

**Casein kinase II phosphorylation site.**

amino acids 65-69

**Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

**N-myristoylation site.**

amino acids 69-75, 188-194

**Amidation site.**

amino acids 58-62

**HBGF/FGF family signature.**

amino acids 103-128

## **FIGURE 12**

ACTTGCCATCACCTGTTGCCAGTGTGGAAAATTCTCCCTGTTGAATTTCATGGAG  
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAAGACAGCAGGGAGATTATTTAC  
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT  
CATTGGATTTGCTGTTATTTTTCTTTCTTTCCCACCAATTGTATTTAT  
TTCCGTACTTCAGAA**AT**GGCCTACAGACCACAAAGTGGCCAGCCATGGGCTTTCT  
GAAGTCTGGCTTATCATTCCCTGGGGCTCTACTCACAGGTGTCAAACCTCTGGCTGCC  
CTAGTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTGACCTCAGTG  
CCTCTGGGATCCCAGGGCGTAACCGTACTCTACCTCCACAACAAACAAATTAAATGC  
TGGATTCCTGCAGAACTGCACAATGTACAGTCGGTGACACGGCTACCTGTATGGCAACC  
AACTGGACGAATTCCCCATGAACCTTCCAAGAAATGTCAAGAGTTCTCCATTGCAAGGAAAC  
AATATTCAAGACCAATTTCACGGCTGCTTGCCCCAGCTTGAAAGCTTGAAGAGCTGCACCT  
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGCTTCCGGGAGGCTATTAGCC  
TCAAATTGTTGTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTGTGGAC  
TTGCAAGAGCTGAGAGTGGATGAAATCGAATTGCTGTCAATATCCGACATGGCCTCCAGAA  
TCTCACGAGCTTGGAGCGTCTTATTGAGGGAACCTCCTGACCAACAAAGGTATGCCG  
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCATTTGACGTAATTGCTGTCC  
CACCCCTCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAAGGACAACAGAT  
AAACCACATTCTTGACAGCCTCTCAAATCTGCTAACGCTGGATATATCCA  
ACAACCAACTGCGGATGCTGACTCAAGGGTTTGATAATCTCTCAACCTGAAGCAGCTC  
ACTGCTCGGAATAACCCCTGGTTGTGACTGCAGTATTAAATGGGTACAGAAATGGCTCAA  
ATATATCCCTTCATCTCAACGTGCGGGTTCATGTGCCAAGGTCTGAACAAAGTCCGG  
GGATGGCCGTCAAGGAATTAAATATGAATCTTGTCCCTGCCCACACGACCCCCGGCCTG  
CCTCTCTCACCCAGCCCCAAGTACAGCTTCTCGACCAACTCAGCCTCCCACCCCTCTAT  
TCCAAACCTAGCAGAAGCTACAGCCTCCAACCTCCTACCACATCGAAACTTCCCACGATT  
CTGACTGGGATGGCAGAGAAAGAGTGAACCCACCTATTCTGAACGGATCCAGCTCTATC  
CATTGTTGAATGATACTTCAAGTCAGCTGGCTCTCTCTTCAACCGTGATGGCATA  
CAAACTCACATGGGTAAAATGGCCACAGTTAGTAGGGGACATGTTCAAGGAGCGCATAG  
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT  
TGTTAGTGCCACTGGATGTTAACTACCGCGCGGTAGAAGACACCATTGTTCAAGGGC  
CACCACCCATGCCTCTATCTGAACAAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA  
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTTGATGGGGCGCGGTGATATT  
GTGCTGGTGGTCTTGCTCAGCGTCTTGCTGGCATATGCACAAAAGGGCGCTACACCTC  
CCAGAAGTGGAAATACAACCGGGCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA  
AGGACAACCTCCATCCTGGAGATGACAGAAACCAAGTTTCAGATCGTCTCTTAAATAACGAT  
CAACTCCTAAAGGAGATTCAGACTGCAGCCATTACACCCAAATGGGGCATTAATT  
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC  
ACTGCCATAC**TGAC**AGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA  
CACACTCGTGTGACATAAAAGACACCGCAGATTACATTGATAAAATGTTACACAGATGCAT  
TTGTCATTGAATACTCTGTAATTATACGGTGTACTATATAATGGGATTAAAAAGTG  
CTATCTTCTATTCAAGTTAATTACAAACAGTTGTAACCTTGTCTTTAAATCTT

## **FIGURE 13**

MGLQTTKWPShGaffLKSwlIISLGLySQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP  
EGVTvLYLHNNQINNAGFPaelHNvQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI  
SRAALAQLLKLEELHDDNSISTVGVEDGAFREAIISLKLFLSKNHLSVPVGLPVDLQELR  
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGlAEGTFSHTKLKEFSIVRNSLSHPPPD  
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQRLMLTQGVFDNLNSNLKQLTARN  
PWFCDCS1KWVTEWLKYIPSSLNVRGFMCGPEQVRGMAVRELMNLLSCPTTPGLPLFTP  
APSTASPTTQPPTLSIPNPSRSYTPPTSKLPTIPDWDGRERVTppI SERIQLSIHFVND  
TSIQVSWLSLFTVMAKLTWVKGHSIVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL  
DAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLLV  
LSVFCWHMHKKGRYTSQKWKYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNNDQLKG  
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639

**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

## FIGURE 14

ACITGGAGCAAGCGCGGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGCTCCGTCTCGCCTCCCACGAGCG  
ATCCCCGAGGAAGGCCGGCCCTCGCGAGGCAGAGGCCAGAGGAAGACCCGGGTGGCTCGCAGGCC  
TCGCTTCCCAGGCCGGCGCTGCAGCCTGCCCCTCTGCTCGCTTGAAATGGAAAAGATGCTCGCAGGCT  
GCTTCTGCTGATCCTCGACAGATCGTCTCCTCCCTGCCAGGGCAGGGAGCGGTACGTGGGAGGTCCATCT  
CTAGGGCAGACAGCTCGGACCCACCCGAGACGGCCCTCTGGAGAGTCTGTGAGAACACAAGCAGGCC  
TGGTTTCATCATGACAGCTCTCGCAGTGTCAAACACCCATGACTATGCAAAGGTCAAGGAGTTCATCGTGGACA  
TCITGCAATTCTTGACATTGGTCTGTGTCACCCGAGTGGGCTGCTCCAATATGGCAGCACTGTCAAGAACATG  
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGGAGCTGTCAGAGGATGCCATCTGTCCACGG  
GCACCATGACTGGGCTGGCATCCAGTATGCCCTGAACATCGCATTCTCAGAGCAGAGGGGGCCGGCC  
GGGAGAATGTGCCACGGGCATAATGATCGTACAGATGGGAGACCTCAGGACTCCGTGGCCAGGTGGCTGCTGA  
AGGCACGGGACACGGGCATCCTAATCTTGCCATTGGTGTGGCCAGGTAGACTCAACACCTTGAAGTCCATTG  
GGAGTGAGCCCCATGAGGACCATGTCITCCTGTGGCCAATTTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC  
AGAAGAAGTTGTGACGGGCCACATGTGCAGCACCTGGAGCATACTGTGCCACTTCTGCATCAACATCCCTG  
GCTCATACGTCTGCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTGT  
GTGCCATGGAGGACCAACTGTGAGCAGCTGTGTGAATGTGCCGGCTCTCGTCTGCCAGTGCTACAGTG  
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGGCTGTGGACTACTGTGCCCTCAGAAAACCACGGATGTGAAC  
ATGAGTGTGAAATGCTGATGGCTCTACCTTGCCAGTGCATGAAGGATTGCTCTTAACCCAGATGAAAAAA  
CGTGACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT  
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGAAAACCTGCAGCCAGTGGACACTGTGAC  
AGCAGGACCATGGCTGTGAGCAGCTGTGTGAACACCGAGGATCCCTCGTCTGCCAGTGCTCAGAAGGCTTCC  
TCATCAACGAGGACCTCAAGACCTGCTCCGGTGGATTACTGCCCTGCTGAGTGACCATGGTTGTGAATACTCCT  
GTGTCAACATGGACAGATCCTTGCTCTGCACTGTGCTGAGGACACGTGCTCCGCAGCGATGGGAAGACGTGTG  
CAAATGGACTCTTGTGCTCTGGGGACCACGGTTGTGAACATTGTGTGAAGCAGTGAAAGATTGTTGTGT  
GCCAGTGTGTTGAAGGTTATATACTCCGTGAACATGGAAAACCTGCAGAAGGAAAGATGTCTGCCAGCTATAG  
ACCATGGCTGTGAACACATTGTGTGAACAGTGCAGACTCATACACGTGCGAGTGTGCTTGAGGGATCCGGCTCG  
CTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTCTGCAATCAACCCACATGGCTGCCAACACATTGTGTTA  
ATAATGGGAAATTCTACATCTGCAATGCTCAGAGGGATTGTTCTAGCTGAGGACGGAAGACGGTGTCAAGAAAT  
GCACTGAAGGCCAACATGACCTGGCTTTGTGATGGATCCAAGAGTCTGGAGAAGAGAATTGAGGTG  
TGAAGCAGTTGTCACTGAAATTATAGATTCTTGACAATTCCCCAACAGCCGCTCGAGTGGGCTGCTCCAGT  
ATTCCACACAGGTCCACACAGAGTCACTCTGAGAAACTTCAACTCAGCCAAGACATGAAAAAACCGTGGCCC  
ACATGAAATACATGGGAAAGGCTCTAGACTGGCTGGCCCTGAAACACATGTTGAGAGAAGTTTACCCAAG  
GAGAAGGGGCCAGGCCCTTCCACAAGGGTGCCAGAGCAGCCATTGTTGACCGACGGACGGCTCAGGATG  
ACGTCCTCGAGTGGGCCAGTAAAGCCAAGGCCATGGTATCACTATGTATGCTGTTGGGCTAGGAAAAGCCATG  
AGGAGGAACATACAAGAGATTGCCCTGAGCCCACAAACAAGCATCTTCTATGCCAACAGACTCAGCACAATGG  
ATGAGATAAGTAAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG  
CAGGGAACTGCCAACCGGCTAACAGCCAACAGAAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT  
CCTGTTCTAATTTCAGTGCAACACAGATATCTGTTGAAGAAGACAATCTTACGGTCTACACAAAAGCTT  
CCCATTCAACAAACCTTCAGGAAGCCCTTGAAGAAAACAGCATCAATGCAAATGTGAAAACCTTATAATGT  
TCCAGAACCTTGCAACAGAACAGTAAGAAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAACGGCC  
TGGAAAATGCCCTGAGATAACAGATGAAGATTAGAAATGCGACACATTGTTAGTCATTGTATCACGATTACAAT  
GAACGCAGTGCAAGGCCAACAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAAACAATCAGTACTGA  
GAAACCTGGTTGCCACAGAACAAAGACAAGAACAGTATACTACTAACTGTATAAATTATCTAGGAAAAAAATCCT  
TCAGAATTCTAACAGATGAATTACCAAGGTGAGAACAGTATGCAAGGTATTGTTGAAATATACTGTGGACAC  
AACTTGCTCTGCCCTACCTGCTTAGTGTGCAATCTCATTGACTATACGATAAAAGTTGACAGTCTTACTT  
CTGTAGAACACTGCCATAGGAATGCTGTTTTGTACTGGACTTACCTTGATATGTATATGGATGTATG  
CATAAAATCATAGGACATATGTACTTGGAACAAGTTGATTTTATAACATATTAAACATTCACCACTTCAG

## **FIGURE 15**

MEKMLAGCFLLILGQIVLLPAEARERSGRSISRGRHARTHPOQTALLESSCENKRADLVFII  
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV  
KMRHLSTGTMGLAIQYALNIAFSEAEGLPLRENVPRVIMIVTDGRPQDSVAEVAAKARD  
TGILIFAIQVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN  
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA  
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKGPGC  
EHECVNMEESYYCRCHRGYTLDPNGKTCRSVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI  
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSRGKTCAKLDSCALGDHGCE  
HSCVSSEDSFVCQCFCFGYILREDGKTCRRKDVCQAIDHGCEHI CVNSDDSYTCECLEGFRLA  
EDGKRCRRKDVKSTHHGCEHICVNNNGNSYICKCSEGFLAEDGRRCKCTEGPIDLVFVID  
GSKSLGEENFEVVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRFNSAKDMKKA  
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN  
GITMYAVGVGKAIEEELQEIASEPTNHLFYAEDFSTMDEISEKLKKGICEALEDSDGRQDS  
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPL  
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 115-119, 606-610, 892-896

**Casein kinase II phosphorylation site.**

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,  
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,  
781-785, 819-823, 866-870

**N-myristoylation site.**

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,  
639-645, 690-696, 752-758, 792-798

**Amidation site.**

amino acids 314-318, 560-564, 601-605

**Aspartic acid and asparagine hydroxylation site.**

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,  
540-546, 581-587

## **FIGURE 16**

GGAGCCGCCCTGGGTGTCAAGCGGCTCGGCTCCCGCGCACGCTCCGGCGTCGCAGGCCCG  
GCACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCGTACTCCGTCCCGCCAGGGAGGGC  
**CATG**ATTCCTCCCTCCCGGGCCCGTGGTACCAACTTGCTGCCTGGTTTTGTTCTGGGCTGA  
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCGCCAACCGGTTGCAG  
GCGGTGGAGGGAGGGAAAGTGGTCTTCCAGCGTGGTACACCTTGACACGGGAGGGTGTCTTC  
ATCCCAGCCATGGGAGGTGCCCTTGATGTGGTCTTCAAACAGAAAGAAAAGGAGGATC  
AGGTGTTGTCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC  
ATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCTA  
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATAAAACCT  
TAGAACTCAATGTACTGGTCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT  
GTGGGGCAAACGTGACCCCTGAGCTGCCAGTCTCAAGGAGTAAGCCCCTGTCCAATACCA  
GTGGGATCGGCAGCTTCCATCCTCCAGACTTCTTGACCCAGCATTAGATGTCATCCGTG  
GGTCTTAAGCCTCACCAACCTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC  
AATGAGGTGGGCAGTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCTGGAGCTGC  
AGTGGTTGCTGGAGCTGTTGTTGACCTGGTGGACTGGGTTGCTGGCTGGCTGGTCC  
TCTTGTACCAACGCCGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC  
ATTGCTCCCCGGACCCCTGCCCTGGCCAAGAGCTCAGACACAATCTCAAGAATGGGACCC  
TTCCTCTGTCACCTCCGCACGAGCCCTCCGGCCACCCATGGCCCTCCAGGCCTGGTGCAT  
TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT  
GGGCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG  
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCAGAGTCAGACTGGCTCTGGTAT**TGATGAC**  
CCCACCACTATTGGCTAAAGGATTGGGTCTCTCCTATAAGGGTCACCTCTAGCAC  
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCAACCTCTC  
TTTACTGTGGAAAACCCTCACTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGAGGAGCCTCCACCCACCCCTGACTCCTCCTATGAAGGCCAGCTG  
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTGAGTCTCCAGGC  
CCCCCTGATCTGACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGT  
ATTGATATAACCTGTCAGGCTGGCTGGTTAGGTTACTGGGCAGAGGATAGGAAATCTC  
TTATTAAAACATGAAATATGTGTTGTTCTATTGCAAATTAAATAAGATACTAA  
TGTTGTATGAAAAA

## **FIGURE 17**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHL PANRLQAVEGGEVVLPAWYTLHGEVSS  
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGQEKDSGPY  
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQ  
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTACQCNVTLEVSTGPGAA  
VVAGAVVGTIVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKSSDTISKNGTL  
SSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSR  
MGAVPVMVPAQSQAGSLV

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 245-267



**N-glycosylation site.**



amino acids 108-112, 169-173, 213-217, 236-240, 307-311



**N-myristoylation site.**



amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370



**Prokaryotic membrane lipoprotein lipid attachment site.**



amino acids 164-175

## **FIGURE 18**

CGCCACCACTCGGGCCACGCCAATGAAACGCCTCCGCTCTAGGGTTTTCCACTTG  
TTGAATTGTCCTATACTCAAAATTGACCCAAGACACCTGTCTCCAAATGAAAATGTGA  
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAA  
TTTGTGAAGATGATAATGAATGTGAAATTAACTCAGTCCTGTGGCAAATGCTAATTGC  
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTCAGATCCAGCAGTAACCA  
AGACAGGTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAATGCCATT  
TAGATAATGTCTGTATAGCTGCAAATATTAATAAAAATTAAACAAAATCAGATCCATAAAA  
GAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA  
TATAATTACATATATAGAAATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAAACA  
CTATCTCAGCCAAGGACACCCCTTCTAACTCAACTCTTACTGAATTGTAAAAACCGTGAAT  
AATTGGTCAAAGGGATACATTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC  
ACATCTTACAAAATCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC  
AAAAGACCACAGAGTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTCTTTGAT  
TCATATAACATGAAACATATTCACTCCATATGAATATGGATGGAGACTACATAAATATA  
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGAGTTGCATTTCATTTATATA  
AGAGTATTGGCCTTGCTTCATCATCTGACAACCTCTTATTGAAACCTCAAATTATGAT  
AATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAAACCC  
ACCCACATTATATGAACCTGAAAAATAACATTACATTAAGTCATGAAAGGTACAGATA  
GGTATAGGAGTCTATGTGCATTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT  
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT  
GACACATTGCAATTGATGTCCTCTGGCCTTCATTGGTATTAAAGATTATAATATTC  
TTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTGCTTGCCATATGCATTTT  
ACCTCTGGTCTTCAGTCAAAGCACCAGGACAACAATTCACAAAAATCTTGCTG  
TAGCCTATTCTTGCTGAACTGTTTCTTGTGGATCAATACAAATACTAATAAGCTCT  
TCTGTTCAATCATTGCCGACTGCTACACTACTCTTTAGCTGCTTGCATGGATGTGC  
ATTGAAGGCATACATCTCATCTCATGTTGGGTGTCATCTACAACAAGGGATTTGCA  
CAAGAATTTTATATCTTGCTATCTAACGCCAGCCGTGGTAGTTGGATTTCCGCAGCAC  
TAGGATACAGATATTATGGACAAACAAAGTATGTTGGCTTAGCACCGAAAACAACATTATT  
TGGAGTTTATAGGACCAAGCATGCCTAATCATTCTGTTAATCTCTGGCTTGGAGTCAT  
CATATACAAAGTTTCGTACACTGCAGGGTGAAACCAGAAGTTAGTTGCTTGAGAAC  
TAAGGTCTTGCAAGAGGAGCCCTCGCTCTCTGTTCTCGGCACCACCTGGATCTT  
GGGTTCTCCATGTTGACCGCATCAGGTTACAGCTTACCTCTCACAGTCAGCAATGC  
TTTCAGGGATGTTCATTTTATTCTGTGTTTATCTAGAAAGATTCAAGAAGAAT  
ATTACAGATTGTTCAAAATGTCCTGTTGGATGTTAAGGTAAACATAGAGAATG  
GTGGATAATTACAACGTGACAAAAATAAAATTCAAGCTGTGGATGACCAATGTATAAAA  
TGACTCATCAAATTATCCAATTATTAACACTAGACAAAAAGTATTTAAATCAGTTTCT  
GTTTATGCTATAGGAACGTAGATAATAAGGTTAAATTATGTATCATATAGATATACTATGT  
TTTCTATGTGAAATAGTTCTGTCAAAATAGTATTGCAAGATATTGAAAGTAATTGGTT  
CTCAGGAGTGTATCACTGCACCCAGGAAAGATTCTTCTAACACAGAGAAGTATATGAA  
TGTCTGAAGGAAACCACTGGCTGATATTCTGTGACTCGTGTGCCTTGAAACTAGTCC  
CCTACCACCTCGGTAAATGAGCTCATTACAGAAAGTGGAACATAAGAGAATGAAGGGCAGA  
ATATCAAACAGTAAAAGGAATGATAAGATGTATTGAAACTGTTTCTGTAGAC  
TAGCTGAGAAATTGTTGACATAAAATAAGAATTGAAGAAACACATTACCAATTGAA  
TTGTTCTGAACCTAAATGTCCACTAAAACAACCTAGACTCTGTTGCTAAATCTGTTCTT  
TTCTAATATTCTAAAAAAAGGTTACCTCCACAAATTGAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 19**

MKRLPLLVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC  
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENVNANCHLDNVCIAA  
NINKTLTKIRSIKEPVALLQEYVRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL  
SNSTLTFEVKTVNNFVQRDTFVVWDKLSVNHRRTLTKLMHTVEQATLRIQSFKTTEFDT  
NSTDIALKVFVFFDSYNMKHIHPHMNMDGYINIFPKRKAAYDSGNVAVAFLYYKSIGPLLS  
SSDNFLLPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAF  
WNYSPDTMNGSWSSEGCELTYSNETHTSCRNCNLTHFAILMSSGSPSIGIKDYNILTRITQLG  
IIISLICLAI CIFTFWFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFC SIIAGL  
LHYFFLAFAFWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFSAA LGYRYYGT  
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA  
LALLFLLGTTWIFGVVLHVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV  
PCCFGCLR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,

648-664

**N-glycosylation site.**

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,  
188-192, 249-253, 381-385, 395-399

**Glycosaminoglycan attachment site.**

amino acids 49-53

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 360-364

**Casein kinase II phosphorylation site.**

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,  
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,  
346-350, 608-612

**Tyrosine kinase phosphorylation site.**

amino acids 36-44, 669-677, 670-678

**N-myristoylation site.**

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,  
434-440, 480-486, 521-527

**Aspartic acid and asparagine hydroxylation site.**

amino acids 75-87

## **FIGURE 20**

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTTCCAAAGNG  
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT  
TGGTCCCTTGCTTCATCATCTGACAACCTTATTGAAACCTCAAAATTATGATAATTCT  
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC  
ATTATATGAACTTGAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA  
GGAGTCTATGTGGCATTGGAAACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG  
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA  
TTTGCAATTGATGTCCTGGCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA  
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTTACCTC  
TGGTTCTCAGTGAATTCAAAGCACCAGGA

## **FIGURE 21**

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGTGGGGAGGAGTCCCCGAAACCCGGCCG  
CTAAGCGAGGCCTCCCTCCCGCAGATCCGAACGGCTGGGCGGGTACCCCGCTGGGA  
CAAGAAGCCGCCCTGCCTGCCGGGGGGAGGGGGCTGGGCTGGGCGGGAGGCAG  
GGTGTGAGTGGGTGTGCGGGGGCGGAGGCTTGTGCAATCCGATAAGAAATGCTCGGG  
TGTCTTGGGCACCTACCGTGGGCCGTAAGGCCTACTATATAAGGCTGCCGCCGGAG  
CCGCCGCCGTCAAGAGCAGGAGCGCTGCCAGGATCTAGGGCACGACCATCCAAACCC  
GGCACTCACAGCCCCCAGCGCATCCGGTCCGCCAGCCTCCGCACCCCCATGCCGG  
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGGTGGTCCACGTATGG  
ATCCTGGCCGGCCTCTGGCTGGCGTGGCCGGCGCCCCCTCGCTTCTCGGACGCCGGGCC  
CCACGTGCACTACGGCTGGGCGACCCCATCCGCCTGCCACCTGTACACCTCCGGCCCC  
ACGGGCTCTCCAGCTGCTTCTGCCATCCGTGCCAGGGCGTGTGGACTGCCGCCGG  
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTCTGCCACCGTGGCATCAAGGG  
CGTGCACACGGTGCACCTCTGCATGGGCCCGACGGCAAGATGCAGGGCTGCTTCAGT  
ACTCGGAGGAAGACTGTGCTTCAGAGGAGGATCCGCCAGATGGCTACAATGTGTACCGA  
TCCGAGAACGCCCTCCGGTCTCCCTGAGCAGTGCCAAACAGCGGAGCTGTACAAGAA  
CAGAGGCTTCTTCACTCTCTCATTTCTGCCATGCTGCCATGGTCCCAGAGGAGCCTG  
AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTTCGCCCTGGAGACCGACAGCATG  
GACCCATTGGCTTGTCAACGGACTGGAGGCCGTGAGGAGTCCAGCTTGAGAAGTAAC  
GAGACCATGCCGGCCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGGACG  
TGCTTCTACAAGAACAGTCTGAGTCCACGTTCTGTTAGCTTAGGAAGAACATCTAGAA  
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCAGTTCTAGCCAATAGACTGTCTGAT  
CATAAACATTGTAAGCCTGTAGCTTGCCTGCCAGCTGCTGCCCTGGGCCCTATTCTGCTCCCTCGA  
GGTTGCTGGACAAGCTGCTGCACTGCTCTGAGTTCTGCTGAATACCTCCATCGATGGGGAAC  
TCACCTCCTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTCCTCATCACTTC  
CCCAGGAGCAGCCAGAACAGCAGGAGTAGTTTAATTTCAGGAACAGGTGATCCACTCTGTA  
AAACAGCAGGTAAATTCACTCAACCCATGTGGAAATTGATCTATCTACTTCCAGGG  
ACCATTGCCCTCCAAATCCCTCCAGGCCAGAACACTGACTGGAGCAGGCATGCCACCAG  
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGACAACTTGAGAATTCCCC  
CTGAGGCCAGTTGTCAATTGATGCTGCTGAGAATAACTTGCTGTCCGGTGTACCTGC  
TTCCATCTCCAGGCCACCAGCCCTTGCCCACCTCACATGCCCTCCCATGGATTGGGCCT  
CCCAGGCCCCCACCTTATGTCAACCTGCACTCTGTTCAAAAATCAGGAAAGAAAAGAT  
TTGAAGACCCCAAGTCTGTCAATAACTTGCTGTGGAGCAGCGGGGGAGACCTAGAAC  
CCTTCCCCAGCACTGGTTCAACATGATATTATGAGTAATTATTGATATGTACA  
TCTCTTATTTCATTATGCCCCAAATTATATTATGATGTAGTAAAGTGAGGTTG  
TTTGTATATTAAAATGGAGTTGTTGT

## **FIGURE 22**

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI  
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE  
EIRPDGYNVYRSEKHLRPLVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD  
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

**Signal peptide:**

amino acids 1-22

**Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

**N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

© 2000 - 2001

## **FIGURE 23**

CCCAGAAGTCAGGGCCCCGGCCTCCTGCCTGCCTGCCGCCGGACCCCTGACCTCCTCA  
GAGCAGCCGGCTGCCGCCGGAAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTGCTG  
CTGCTGCCTACCTGGTGGTCGCCCTGGCTATCATAAGGCCTATGGGTTTCTGCCAA  
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAAAACCCAA  
AGAAGACTGTTCTCCAGATTAGAGTGGAGAAACTGGTCGGAGTGTCTCCTTGTCTAC  
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG  
GATCAAAATGTGACAAGAAGTGTGATGCCGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG  
AGCAAGGCCAAACCTGGAAGAGGATACAGTCAGTCACTCTGGAAAGTATTAGTGGCTCCAGCAGTT  
CCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA  
CAAAGAAGGGAAATCCAGCTCTGAATACACATGGTTAAGGATGGCATCCGTTGCTAGAAA  
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAATGAATAACAAAAACTGGAAC  
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCTGTGAAGCCCGCAATT  
TGTTGGATATCGCAGGTGTCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA  
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTCCGTTGTGGCCTGGTGTATGCTAT  
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA  
AGCCACGACAATGAGTGGAAAATGTGCAGTGGCTCACGCCGTAAATCCAGCACTTGGAGG  
CCGGCGGGCGGATCACGAGGTCAAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAACCC  
CATCTCTACTAAAATACAAAAATTAGCTGGCATGGTGGCATGTCCTGCAGTTCCAGCTGC  
TTGGGAGACAGGAGAATCACTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC  
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAATAAAATAAAATA  
AATAAAATCTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

## **FIGURE 24**

MARRSRHRLLLLLLRLVVALGYHKAYGFSAPKDDQQVVTAVEYQEAILACKTPKTVSSRLE  
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNL  
EEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKD  
GIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARN  
SVGYRRCPGKRMQVDDLNISGIIAAVVVA  
LVI  
SVCGLGV  
CYAQRKGYFSK  
ETSFQKS  
NSSSK  
ATTMSE  
NVQWL  
TPV  
IPALW  
KAAAGGS  
RGQEF

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 130-144, 238-258

**N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

**Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

**N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

**Amidation site.**

amino acids 226-230

## **FIGURE 25**

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG  
AAAGAAGAGGAAGATGTTGGCAACATTTATTAACATGCTCACAGCCGGACCCCTGGCAT  
CATGCTGCTATTCTGCAAATACTGAAGAAGCATGGGATTAAATATTTACTCTAAATAA  
ATGAATTACTCAATCTCTATGACCATCTATACATACTCCACCTCAAAAAGTACATCAATA  
TTATATCATTAAGGAAATAGTAACCTCTTCTCAATATGCATGACATTTGGACAATG  
CAATTGTGGCACTGGCACTTATTCAGTGAAGAAAAACTTGTGGTTATGGCATTCA  
TTGACAAATGCAAGCATCTCCTATCAATCAGCTCTATTGAACTTACTAGCACTGACTG  
TGGAATCCTAAGGGCCATTACATTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT  
CCGAATTCACTGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAG  
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTGGTTACACCCAGATCCATTAT  
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACTTCCCAGCCAGATTGCC  
AGCTAACACACAGATTCTCTCACAGACTAACAAATTGCAAAAATTGAATACTCCACAG  
ACTTCCAGTAAACCTACTGGCCTGGATTATCTCAAAACAATTATCAGTCACCAAT  
ATTAATGTAAGGAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAACAAACTACTGA  
ACTGCCTGAAAAATGTCGTCCGAACGTGAGCAACTACAAGAACTCTATATTAACTACA  
TGCTTCTACAATTCACCTGGAGCCTTATTGGCCTACATAATCTTCTCGACTTCATCTC  
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTCAAATCTAGAGAT  
TCTGATGATTGGGAAAATCCAATTATCAGAACTCAAAGACATGAACTTTAAGCCTTATCA  
ATCTTCGAGCCTGGTTAGCTGGTATAAACCTCACAGAAATACAGATAACGCCCTGGTT  
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGCTTATTAAAGTACCCCATGT  
TGCTCTCAAAAGTGTAAATCTCAAATTGGATCTAAATTAAACCTATTAAATAGAA  
TACGAAGGGGTGATTTAGCAATATGCTACACTAAAGAGTTGGGGATAAAATAATATGCCT  
GAGCTGATTTCCATCGATAGTCTGCTGTGGATAACCTGCCAGATTAAAGAAAATAGAAGC  
TACTAACACCCCTAGATTGTCTTACATTCAACCCCAATGCATTTCAGACTCCCCAAGCTGG  
AATCACTCATGCTGAAACAGCAATGCTCAGTGCCTGTACCATGGTACCATGGTACCTG  
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTGACTGTGTCATCCGTG  
GATGAACATGAACAAAACCAACATTGGATTCAAGGAGCCAGATTCACTGTTTGCCTGGACC  
CACCTGAATTCCAAGGTCAAATGTTGGCAAGTGCATTTCAGGGACATGATGGAAATTGT  
CTCCCTCTTATAGCTCCTGAGAGCTTCTTCTAAATCTAAATGTAAGAGCTGGAGCTATGT  
TTCCTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTCTG  
GTCAAAAACCTTGCCTAATACCCGTACAGACAAGTTCTATGTCCATTCTGAGGGAAACACTA  
GATATAATGGCGTAACTCCCAAAGAAGGGGTTATATACTTGTATAGCAACTAACCTAGT  
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAAATG  
GCTCTTGAATATTAAGAGATATTCAAGGCAATTCACTGTTGGTGTCTGGAAAGCA  
AGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA  
TGCTCGCAAAGTGTGAAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC  
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTATCAGAAAAACAGAAAAAAA  
TGTGTAAATGTCACCACCAAGGTTGCACCCCTGATCAAAAAGAGTATGAAAAGAATAATAC  
CACAAACACTTATGGCCTGTCTGGAGGCCTCTGGGGATTATTGGTGTGATATGTCTTATCA  
GCTGCCTCTCCAGAAATGAACGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG  
AAACCAACCTTGCATTAGGTGAGCTTATCCTCTGTATAAATCTCTGGAAAGCAGGAAA  
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTAGGTTACCAACAAATATGTCT  
AAAAACCAAGGAAACCTACTCCAAAATGAAC

## **FIGURE 26**

MKDMPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRTSIYMEASTVDCNDLGLLT  
FPARLPANTQILLQTNNIAKIEYSTDFTPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE  
ENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLLRLHLSNRQLQMINSKWFDA  
LPNLEILMIGENPIIRIKDMNFKPLINLRSVIAGINLTEIPDNALVGLENLESISFYDNRL  
IKVPHVALQKVVNLKFLLDNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSLAVDNLPD  
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSAHYHTIESLPNLKEISIHSNPIRC  
DCVIRWMNMNKTNIRFMEPDSDLFCVDPPEFQGQNRQVHFRDMMEICLPLIAPESFPSNLNV  
EAGSYVSFHCRTAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTC  
IATNLVGAIDLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV  
KTENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE  
YEKNNTTTLMACLGGLLGIIGVICLISCLSPEMNCDGGHSYVRNYLQKPTFALGELYPP LIN  
LWEAGKEKSTSLKVKATVIGLPTNMS

**Signal sequence:**

amino acids 1-22

**Transmembrane domain:**

amino acids 633-650

**N-glycosylation site.**

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

**Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

**Tyrosine kinase phosphorylation site.**

amino acids 570-579

**N-myristoylation site.**

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

**Cell attachment sequence.**

amino acids 277-280

## **FIGURE 27**

GCCCCGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC  
CACGCTTGTGGAGTAGATGAGGAATGGCTCGTATTATGCTGACATTCCAGCATGAATCT  
GGTAGACCTGTGGTTAACCGTTCCCTCCATGTGTCTCCTCCTACAAAGTTGTTCTTA  
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTCTTCTG  
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG  
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT  
GCCTTCAAAGGAGTAGCTGAAACCTTGCAAGACTCTGGACTTGTCCGACAATCGGATTCAAAG  
TGTGCACAAAATGCCTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAAACCCCTGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC  
AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC  
AACCGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA  
TGTGGCTGGTTCACTATGGTGTCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG  
GATGCCCGGAGACACCTCGAATAACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA  
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAAACTGACTGTCATTGAGAAAGAAAGAAA  
GTAGTTTGCATTGCAGTAGAAATAAGTGGTTACTTCTCCATCCATTGTAAACATTTGAA  
ACTTGTATTCAGTTTTTGAAATTATGCCACTGCTGAACCTTAACAAACACTACAACA  
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT  
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAATAATGAAATTATTTTTT  
AATTAAAAGCAAATAAAAGCTTAACTTGAACCAGGGAAAAAAAAAAAAAAACA

1000 900 800 700 600 500 400 300 200 100

## **FIGURE 28**

MNLVDLWLTRSLSMC~~LLQSFVLMILCFHSASMC~~PKGCL~~SSGG~~LNVTCSNANLKEIPRDL  
PPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR  
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFL  
NAANDADLCNL~~PKKTTDYAMLVTMFGWFTMV~~ISYVVYYVRQNQEDARRHLEYLKSLPSRQKK  
ADEPDDISTVV

**Signal sequence:**

amino acids 1-33

**Transmembrane domain:**

amino acids 205-220

**N-glycosylation site.**

amino acids 47-51, 94-98

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 199-203

**Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

**N-myristoylation site.**

amino acids 37-43, 45-51, 110-116

## **FIGURE 29**

## **FIGURE 30**

MQVSKRMLAGGVRSMPSPLLACWQPILLLVLGSVLSGSATGCPRCECSAQDRAVLCHRKCF  
VAVPEGIPETRLLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTL  
GLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFDQLYNLKSLEVDNDLVYISHRA  
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVL  
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSM  
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSVGNLETLL  
CDCRLLWVFRRWRLNFRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKA  
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTVFPDGTL  
CIAANAGGNDNSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGE  
IATTMGFISFLGVVLFCVLFLWSRGKGNTHNIEIEYVPRKSDAGISSADAPRKFN  
MKMI

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 556-578

**N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,  
492-496, 505-509, 526-530, 542-546

**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,  
607-611

**Tyrosine kinase phosphorylation site.**

amino acids 590-598

**N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

## FIGURE 31

CCCACGCGTCCGACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGGCCCTTCGGTCAAC  
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGGCCAGCC  
AGGGAGCCGGCCGGGAAGCGCGATGGGGCCCCAGCCGCTCGCTCCTGCTCCTGCTCCTGC  
TGTCGCTGCTGGCGCCGGGGCAACCTCTCCCAGGACGACAGCCAGCCCTGG  
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTCAAGTGCCAAGTGAAAGATCA  
CGAGGACTCATCCCTGCAATGGCTAACCTGCTCAGCAGACTCTACTTGGGAGAAGA  
GAGCCCTCGAGATAATCGAATTCAAGCTGGTACCTCACGCCAACGAGCTCAGCATCAGC  
ATCAGCAATGTGGCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTCACTATGCCCTGT  
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCATCATCACTGGTT  
ATAAAATCTTCATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTCTGGGAGCAAG  
CCTGCAGCCGGCTCACCTGGAGAAAGGTGACCAAGAACCTCACGGAGAACCAACCGCAT  
ACAGGAAGATCCCAATGGTAAAACCTTCACTGTCAGCAGCTCGTGACATTCCAGGTTACCC  
GGGAGGATGATGGGGGAGCAGTCGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC  
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC  
TCCCCATCCTCGTGGAGGGCCAGAACGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC  
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT  
GCCCTGATCTCCCTTCCTCAACAAAGAGTGAACAGTGGCACCTACGGCTGCACAGCCACCA  
CAACATGGGAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCT  
CCTCCTCCAGCACCTACCACGCCATCATCGTGGGATCGTGGCTTCATTGTCTCCTGCTG  
CTCATCATGCTCATCTTCCCTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA  
TGAGGCAAAGGCTCCGACGATGCTCCAGACGCCAGCGGACAGGCCATCATCAATGCAGAAGGG  
GGCAGTCAGGAGGGAGCACAAGAAGGAATATTCATTAGAGGGCGCTGCCACTCCTGC  
GCCCCCCAGGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA  
CCGCAGGGCCGCCCTCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAAATGTCTGC  
TTTGGGTGCGGTTTGACTCGGTTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGAGGG  
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAACAATCC  
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA  
AACAAAAAACAA

## **FIGURE 32**

MGAPAASLLLLLFFACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLKCQVKDHEDSSLQW  
SNPAQQTLYFGEKRALRDNRQLVTSTPHELYSISISNVALADEGEYTCISIFTMPVRTAKSLV  
TVLGIHQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK  
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ  
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKS DSGTYGCTATSNMGSYKA  
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDD  
APDADTAIINAEGGQSGGDDKKEYFI

**Signal sequence:**

amino acids 1-20

**Transmembrane domain:**

amino acids 331-352

**N-glycosylation site.**

amino acids 25-29, 290-294

**Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

**N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 33**

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTTCTTCTCCTTCTGG  
CTTCGGACATTGGAGCACTAAATGAACCTGAAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG  
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGTTAAAAATGCTGCTTGGATTCTGTT  
GCTGGAGACGTCTTTGTTGCCGCTGGAAACGTTACAGGGGACGTTGCAAAGAGAAGA  
TCTGTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA  
AGTCTGCAGCGTTCACTGCCCGACTTCCCAGTTTACCAATTATTCTGCATGGCAATT  
CCTCACTCGACTTTCCCTAATGAGTTGCTAACCTTATAATGCGGTTAGTTGCACATGG  
AAAACAATGGCTTGCATGAAATCGTCCGGGGCTTTCTGGGGCTGCAGCTGGTAAAAGG  
CTGCACATCAACAACAAGATCAAGTCTTTCGAAAGCAGACTTTCTGGGGCTGGACGA  
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAGACCCGGGGCTTCCAGG  
ACTTGAACAAGCTGGAGGTGCTCATTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC  
GTGTTCCAGTATGTGCCCATACCCACCTCGACCTCCGGGTAACAGGCTGAAAACGCTGCC  
CTATGAGGAGGTCTTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCT  
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC  
CTGATCGGCCAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC  
CACCGAACAGGACTTGTGTCCTTGAAAAACCGAGTGGATTCTAGTCTCCGGCGCCCCCTG  
CCCAAGAACAGAACCTTGCTCCTGGACCCCTGCCAACCTTCAAGACAAATGGCAAGAG  
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT  
CAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCTTAGCTAAC  
GTTTACCCCTGCCCTGGGGCTGAGCTGCGACCACATCCCAGGGTGGGTTAAAGATGAAAC  
TGCAACAAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCCAAGCTCTAACGTGCAGGA  
GCTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTGTGGATTACAAGA  
ACCTCATTCTGTTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACACACTTTCAAG  
AACCTTTGGACCTCAGGTGGCTACATGGATAGCAATTACCTGGACACGCTGTCCCAGGA  
GAAATTGCGGGGCTGCAAAACCTAGAGTACCTGAACAGTGGAGTACAACGCTATCCAGCTCA  
TCCTCCGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAAACAAACCTG  
CTGAGGTCCCTGCCTGTGGACGTGTTCGCTGGGTCTCGCTCTAAACTCAGCCTGCACAA  
CAATTACTCATGTACCTCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATATCCAGA  
TAGACCTCCACGGAAACCCCTGGGAGTGCTCTGCACAATTGTGCCTTCAAGCAGTGGGCA  
GAACGCTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTCTT  
TAGAAAGGATTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT  
CGCCCACGTTAACCTCGCACAGTAAAACAGCACTGGGTTGGCGAGACCGGACGCACCTC  
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGCTCCGGACTGCTGCTGGT  
GTTTGTACCTCCGCCTTCACCGTGGTGGCATGCTCGTGTATCCTGAGGAACCGAAAGC  
GGTCCAAGAGACGAGATGCCAACTCCTCCCGTCCGAGATTAATTCCCTACAGACAGTCTGT  
GAECTTCTACTGGCACAATGGCCTTACAACGCAGATGGGCCACAGAGTGTATGACTG  
TGGCTCTACTCGCTCTCAGACTAAAGACCCAAACCCAAATAGGGAGGGCAGAGGGAAAGGCG  
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCCAAATCCCGCG  
CCATCAGCCTGGATGGCATAAGTAGATAAAACTGTGAGCTCGCACAAACGAAAGGGCT  
GACCCCTACTTAGCTCCCTCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA  
GCCAGCTCGCTTTGCTGAGAGGCCCTTTGACAGAAAGGCCAGCACGACCCCTGCTGGAAG  
AACTGACAGTGCCCTGCCCTCGGCCCCGGGGCTGTGGGTTGGATGCCCGGGTTCTATAC  
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTCCCTGTGGATTAG  
CCCCGTGATGGCTCCCTGTTGGTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT  
TGTAAATAAGTAACCTTGACTCTGAC

## **FIGURE 34**

MLLWILLLETSLCFAAGNVTGVCCKEKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH  
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPG AFLGLQLVKRLHINNNKIKSFRKQ  
TFLGLDDLEYLQADFNLLRDIDPGAFQDLSKLEVLIILNDNLISTLPANVFQYVPI THLDLRG  
NRLKTL PYEVLEQI PGIAEILLEDNPWDCTCDLISLKEWLENIPKNALIGRVVCEAPTRLQ  
GKDINNETTEQDLCPLKNRVDSL PAPPAQEETFAPGPLPTPKTNGQEDHATPGSAPNGGT  
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGCSDHIPGSGLKMNCCNRNVSSLADLKP  
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLLDGNNNIATVENNTFKNLLDLRWLYMDSNY  
LDTLSREKFAGLQNLEYLNVEYNIAIQILPGLTFNAMPKLRILILNNNLLRSLPVDVFAGVSL  
SKLSLHN NYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLMSDLKC  
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHNSYLDTSRVSISVL  
VPGLL VFVTS AFTVVGMLV FILRNRKRSKRDANS SASEINSLQTVCDSSYWHNGPYNADG  
AHRVYDCGSHSLSD

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 618-638

**N-glycosylation site.**

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 122-126, 646-650

**Casein kinase II phosphorylation site.**

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697

**N-myristoylation site.**

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

## **FIGURE 35**

AGTCGACTGCGTCCCCTGTACCCGGGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC  
TGCACCGGGCTGGCAGCGCTCCGCACACATTCTGTGCGGGCTAAGGGAAACTGTTGGC  
CGCTGGGCCCGGGGGGATTCTTGGCAGTTGGGGGTCCGTGGGAGCGAGGGCGGAGGGG  
AAGGGAGGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC  
AGCTCTGCGTCCTCGAGCGGACAGATCCAAGTTGGGAGCAGCTGTGCGTGCAGGGCCTCAG  
**AGAATGAGGCCGGCGTTGCCCTGTGCCCTCTGGCAGGCGCTCTGGCCCGGGCCGGCGG**  
CGGCGAACACCCCCACTGCCGACCGTGTGGCTCGGCTCGGCCCTGGGGCCTGCTACAGCCTGC  
ACCAAGCTACCATGAAGCGGCAGGGCGCCGAGGAGGCTGCATCTGCGAGGTGGGGCGCTC  
AGCACCGTGCCTGCAGCTGCGCCTGTGCTCGCCTCGCAGGGCCAGGCGCAGGCGCAGG  
GCCCGGAGGGGGCTCAAAGACACTGCTGTTCTGGGTGCACGGCTGAGCGCAGGCAGGCGTCCCAGT  
GCACCCCTGGAGAACGAGCCTTGCAGGGTTCTCTGGCTGTCTCCGACCCGGCGGTCTC  
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGGGAGATGCGC  
GGTACTCCAGGCCACCGGTGGGTGAGGCCGAGGCTGGAAGGAGATGCGATGCCACCTGC  
GCGCCAACGGCTACCTGTGCAAGTACCAAGTTGAGGTCTGTGCTCGCCGCGCCCCGGG  
GCCGCCTCTAACTTGAGCTATCGCGCCCTTCCAGCTGCACAGCGCCGCTCTGGACTTCAG  
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCGATCTCAGTTACTTGCA  
TCGCGGACGAAATCGCGCTCGCTGGACAAACTCTCGGGCGATGTGTTGTCCCTGCC  
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAAC TGCCTAGACGACTTGGGAGG  
CTTGCCTGCGAATGTGCTACGGCTTCAGCTGGGAAGGACGGCGCTTGTGACCA  
GTGGGGAGGACAGCCGACCCCTGGGGGACCGGGGTGCCACCAGGCGCCGCCACT  
GCAACCAGCCCCGTGCCGCAGAGAACATGGCAAATCAGGGTCGACGAGAACGCTGGGAGAGAC  
ACCACTGTCCTGAACAAGACAATTCAAGTAACATCTATTCTGAGATTCTCGATGGGAT  
CACAGAGCACGATGTCACCCCTCAAATGTCCCTCAAGCCGAGTCAGCTCCCTGCCACTCCTCAGGCTT  
CCATCAGGGAGCGTGATTTCAAGTTAATTCTACGACTTCTCTGCCACTCCTCAGGCTT  
CGACTCCTCCTCTGCCGTGGTCTTCATATTGTGAGCACAGCAGTAGTAGTGTGTTGATCT  
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCACGAAAGCCCTTCCAGCCA  
AGGAAGGAGTCTATGGGCCGCCGGCTGGAGAGTGATCCTGAGGCCGCTGCTTGGGCTC  
CAGTTCTGCACATTGCACAAACAATGGGGTGAAGTCGGGACTGTGATCTGCCGGACAGAG  
CAGAGGGTGCCTTGCCTGGCGAGTCCCTCTGGCTCTAGTGATGCAT**AGGAAACAGGGGA**  
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACGGGGAACCAAGAGGAACCTAC  
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTCTCAAATTCCCTTACTCCACTGAG  
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA  
TGGTGTGATGACTGGGGACCGGGTAGTGTGCTGGGAGAGATATTCTTATGTTATTGGAGAA  
TTTGGAGAAGTGATTGAACTTTCAAGACATTGGAAACAAATAGAACACAATATAATTACA  
TTAAAAAATAATTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTCAGGCTAGGAGTAT  
ATTGGTTGAAATCCCAGGGAAAAAAATAAAAATTAAGGATTGTTGAT

## FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS  
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGLE  
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPGA  
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG  
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEQPTLGGTGVPTRRPPATA  
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTTSIPEIPRWGSQSTMSTLQMSLQAESKATITP  
SGSVISKFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILMTVLGLVKLCFHESPSSQPR  
KESMGPPGLESDEPAALGSSSAHCTNNGVKVGCDLRDRAEGALLAESPLGSSDA

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 189-193, 381-385

**Glycosaminoglycan attachment site.**

amino acids 289-293

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

**Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

**N-myristoylation site.**

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

**Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

## FIGURE 37

CGGACGCGTGGATTCAAGCAGTGGCTGTGGCTGCCAGAGCAGCTCCTCAGGGAAACTAAG  
CGTCGAGTCAGACGGCACATAATCGCCTTAAAAGTGCCTCCGCCCTGCCGGCGCGTATC  
CCCCGGCTACCTGGGCCCGCCCGCGGGTGCAGCGCTGAGAGGGAGGCCGCCGGCAGCCGA  
GCCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGGTGTGAGCGCGGTGGTGCAGGA  
GGGGCGTGTGTGCCGGCGCGCGCCGGTGGGTGCAAACCCCGAGCGTACGCTGCCATGA  
GGGGCGCGAACGCCCTGGCGCCACTCTGCCTGCTGGCTGCCGCCACCCAGCTCGCGG  
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT  
TATTGGCAGTGAAGGTTTCTGGAGTGTACCCCTCAAATAGCAAATGTACTTGGAAAATCA  
CAGTTCCCAGAGAAAAGTAGTCGTTCTCAATTCCGATTCAAGACCTCGAGAGTGACAAC  
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGCCAGCGCATTGGCCG  
CTTCTGTGGCACTTCCGGCTGGAGCCCTGTGTCCAGTGGCAACAAGATGATGGTGCAGA  
TGATTCTGATGCCAACACAGCTGGCAATGGCTTATGCCATGTTCTCGCTGTAACCA  
AACGAAAGAGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTTTAAAAC  
CCCCAACTGCCAGACCGGGATTACCCCTGCAGGAGTCACTTGTGTGGCACATTGTAGCCC  
CAAAGAATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC  
CGATATGATTATGTGGCTGTGTTAATGGCGGGAAAGTCAACGATGCTAGAAGAATTGGAAA  
GTATTGTGGTGTAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACTTCTTATTAGT  
TTTATCAGACTTAAGTTAATGCAGATGGGTTATTGGTCACTACATATTCAAGGCCAAA  
AAACTGCCTACAACACTACAGAACAGCCTGTCACCACATTCCCTGTAACCACGGGTTAAA  
ACCCACCGTGGCCTGTGTCACAAAAGTAGACGGACGGGACTCTGGAGGGCAATTATT  
GTTCAAGTGACTTTGTTAGGCCGACTGTTATCACAACCACACTCGCGATGGAGTTG  
CACGCCACAGTCTCGATCATCACACATCTACAAAGAGGGAAATTGGCGATTAGCAGGCAGG  
CAAGAACATGAGTGCCAGGCTGACTGTCGTGCAAGCAGTGCCTCTCAGAACAGGTC  
TAAATTACATTATTATGGGCAAGTAGGTGAAGATGGGCGAGGCAAAATCATGCCAACAGC  
TTTATCATGATGTTCAAGACCAAGAACATCAGAACGCTCCTGGATGCCCTAAAAAATAAGCAATG  
**TTAACAGTGA**ACTGTGTCATTAAAGCTGATTCTGCCATTGCCCTTGAAAGATCTATGTC  
TCTCAGTAGAAAAAAATACCTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG  
GACTGGTTGACTCTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAAGTTCTT  
TGCCTGCTGTCAGAGGAGCAGCTATCTGATTGAAACCTGCCGACTTAGTGCAGGTAGAGA  
AGCTAAAAGTGTCAAGCGTTGACAGCTGGAAAGCGTTATTTATACATCTGTAAAAGGAT  
ATTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAAGATTTAGAAGTGCATATTATAGT  
GTTATTGTTCACCTCAAGCCTTGCCTGAGGTGTACAATCTGCTTGCCTTCTA  
AATCAATGCTTAATAAAATTAAAGGAAAAAA

## **FIGURE 38**

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESFIGSEGFPGVYPPNSKCTWK  
ITVPEGKVVVLNFRFIDLESDNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV  
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV  
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGEVNDARRIGKYCGDSPAPIVSERNELLI  
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRGTLEGN  
YCSSDFVLAGTVITTITRD GSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR  
GLNYIIMQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

**Signal sequence:**

amino acids 1-23

**N-glycosylation site.**

amino acids 355-359

**Casein kinase II phosphorylation site.**

amino acids 64-68, 142-146, 274-278

**Tyrosine kinase phosphorylation site.**

amino acids 199-208

**N-myristoylation site.**

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,  
305-311, 309-315, 320-326, 330-336

**Cell attachment sequence.**

amino acids 149-152

## **FIGURE 39**

CGGACGCGTGGCGGACGCGTGGCGCCACGGCGCCGCGGCTGGGGCGGTGCTTCTT  
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG  
GCCTAGTCCCAGCTGTCTGGGCCTCAGCCTCTCCTCAACCTCCCAGGACCTATCTGG  
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTACACTG  
CCGGGGACTGGTTGACAGCTTAACAAGGGCTGGAGAGAACCATCCGGACAACTTGGAG  
GTGGAAACACTGCCTGGAGGAAGAGAATTGTCAAATACAAAGACAGTGAGACCCGCCTG  
GTAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTCGAGTGCCACCGCCTGGAGCT  
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCCCGGACCTTTCC  
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC  
CTTCCCTGTCTGGGGAACAGAGAGGCCCTGGCTACGGCAGTGTGAAGGAGAAGG  
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGTACGGGGTGAGGCCTGTGGCC  
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCATCTGGTATGTTGGCTTGT  
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGGCAATGCAAGAAGGG  
CTGGGCCCTGCATCACCTCAAGTGTGAGACATTGATGAGTGTGGCACAGAGGGAGCCA  
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG  
GCCTGCCTAGGCTGCATGGGGCAGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA  
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTCCGGAGAGA  
ACAAGCAGTGTGAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG  
ATGGAAGGCATCTGTGTAAGGAGCAGATCCAGAGTCAGCAGGCTTCTCTCAGAGATGAC  
AGAAGACGAGTTGGTGGTGCTGCAGCAGATGTTCTTGGCATCATCTGTGCACTGGCCA  
CGCTGGCTGCTAAGGGCACTGGTGTACCGCCATCTCATTGGGCTGTGGCGGCCATG  
ACTGGCTACTGGTGTCAAGAGCGAGTGAACGCTGGAGGGCTTCATCAAGGGCAGAT  
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCGAGAGCTTGGCTGCC  
TCCTGCTGGACACTCAGGACAGCTGGTTATTTGAGAGTGGGTAAGCACCCCTACCTG  
CCTTACAGAGCAGCCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAAGTAGC  
CCTGAAGGTGGATACCATGAGCTTCACTGGCGGGACTGGCAGGCTTCACAAATGTGTGA  
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG  
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCCAGTTCTGT  
TCTGTGTTCACACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAGA  
AAGGTCTTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 40**

MAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER  
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ  
QEAPDLFQWLCSDSLKLCGPAGTFGPSCLPAGTERPCGGYGCCEGEGTRGGSGHCDCQAG  
YGEACGQCGLGYFEAERNASHLVCACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE  
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKCSPGYQQVGSKCLDVDECE  
TEVCPGENKCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG  
IIICALATLAAGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIFKGR

**Signal sequence:**

amino acids 1-29

**Transmembrane domain:**

amino acids 372-395

**N-glycosylation site.**

amino acids 79-83, 205-209

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 290-294

**Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-363

**N-myristylation site.**

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,  
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,  
326-332, 372-378, 395-401

**Aspartic acid and asparagine hydroxylation site.**

amino acids 321-333

**EGF-like domain cysteine pattern signature.**

amino acids 181-193

## **FIGURE 41**

TGAGACCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTGCTCCTCCAGGGCA  
GCACCATGCAGCCCCCTGTGGCTCTGCTGGCACTCTGGGTGTTGCCCTGGCCAGCCCCGGG  
GCCGCCCTGACCAGGGAGCAGCTCCTGGCAGCCTGCTGCCAGCTCAGCTCAAAGAGGT  
GCCCACCCCTGGACAGGGCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAGT  
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTAGCCAGAGC  
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGGTCTGG  
CATGGAGCAGCGCTGCCGCCAACAGCGAGCTGGTCAGGCCGTGCTGCCCTTCCAGG  
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGCGGCTGTCCCGCGCAGGCCCGGGCC  
CGGGTGACCGTCGAGTGGCTGCGCGTCCCGCAGACGGCTCCAACCGCACCTCCCTCATCGA  
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA  
ACTTCTGGCAGCAGCTGAGCCGGCCCGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG  
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTGCCCTCGCAGGGGGC  
GCCAGCCGGCTGGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTGGGACTATGGAG  
CTCAGGGCGACTGTGACCCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG  
ATGTACATTGACCTGCAGGGATGAAGTGGGCCAGAACTGGGTGCTGGAGCCCCCGGGCTT  
CCTGGCTTATGAGTGTGGCACCTGCCGGAGCCCCCGGAGGCCCTGGCCTTCAAGTGGC  
CGTTCTGGGCCTCGACAGTCATGCCCTCGGAGACTGACTCGCTGCCATGATCGTCAGC  
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA  
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCAGGAGGCTCCAGCCATAGGCGCCTAGTG  
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGTGAGGGTACCAAGGAGAGCTG  
GCGATGACTGAAGTGCCTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT  
CCTCTGACAAGTTACCTCACCTAATTTGCTCTCAGGAATGAGAACATTTGGCCACTGGA  
GAGCCCTGCTCAGTTCTATTCTATTACTGCACTATATTCTAACGCACTTACAT  
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCATTGTTACTTGTCCGTAC  
TGGATCTGGCTAAAGTCCTCCACCACCACTCTGGACCTAACGACCTGGGGTTAAGTGTGGGT  
TGTGCATCCCCAATCCAGATAATAAGACTTTGTAAAACATGAATAAACACATTATTCT  
AAAA

## **FIGURE 42**

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLRLQLQLKEVPTLDRADMEELVPIPTHVRAQYV  
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP  
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF  
WQQLSRPRQPLLQSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ  
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF  
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 158-162



cAMP- and cGMP-dependent protein kinase phosphorylation site.



## **FIGURE 43**

GTCTGTTCCCAGGAGTCCTCGCGGCTGTTGTCAGTGGCCTGATCGCGATGGGACAAA  
GGCGCAAGTCGAGAGGAAACTGTTGTCCTCTTCATATTGGCGATCCTGTTGCTCCCTGG  
CATTGGGCAGTGTACAGTGCACCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT  
GTGAAGTTGTCCTGTCCTACTCGGGCTTTCTTCTCCCCGTGAGTGGAGTGGAAAGTTGACCA  
AGGAGACACCAACCAGACTCGTTGCTATAATAACAAGATCACAGCTCCTATGAGGACCGGG  
TGACCTTCTGCCAACTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
ACTTGTATGGTCTCTGAGGAAGGCGAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT  
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTGCCACCATTGGGAACCGGG  
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTTCTGAATAACACCTGGTCAAAGAT  
GGGATAGTGTGATGCCCTACGAATCCAAAAGCACCCGTGCCCTCAGCAACTCTCCTATGTCT  
GAATCCCACACAGGAGAGCTGGTCTTGATCCCCTGTCAAGCTCTGATAACTGGAGAATACA  
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAAGCT  
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTGTAACCCCTGATTCTCCTGGGAAT  
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA  
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCGAAGTGAAGGAGAATTCAAACAG  
ACCTCGTCATTCTGGTGTGAGCCTGGTCGGCTCACCGCCTATCATCTGCATTGCCCTACT  
CAGGTGCTACCGGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCCTATTGTCTTC  
TACACCCCACAGGGCCCCCTACTTCTCGGATGTGTTTAATAATGTCACTATGTGCC  
ATCCTCCTTCATGCCCTCCCTTCCCTACCACTGCTGAGTGGCTGGAACCTGTTAAA  
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC  
TTCTAAAGTAGACAGAAAAATGGCGGGGTGCAAGGAATCTGCACTCAACTGCCACCTGGC  
TGGCAGGGATCTTGAATAGGTATCTTGAGCTGGTCTGGCTCTTCCCTGTACTGAC  
GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTGG  
TGATGACACTGGGTCTTCCATCTCTGGGCCACTCTCTGTCTTCCATGGGAAGTG  
CCACTGGGATCCCTCTGCCCTGCTCTGAATACAAGCTGACTGACATTGACTGTCTGT  
GGAAAATGGGAGCTCTGTTGGAGAGCATAGTAAATTTCAAGAGAACTTGAAGCCAAAAG  
GATTAAAACCGCTGCTCTAAAGAAAAGAAAAGCTGGAGGCTGGCGCAGTGGCTACGCC  
TAATCCCAGAGGCTGAGGCAGGCAGGATCACCTGAGGTGGAGTTGGGATCAGCCTGACCA  
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCGTAGTC  
CCAGCTGCTCAGGAGCCTGGCAACAAAGAGCAAAACTCCAGCTCAAAAAAAA

## **FIGURE 44**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEW  
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV  
KLIVLVPPSKPTVNIPSSATIGNRAVLTSEQDGSPPPSEYTWFKDGIVMPTNPKSTRAFSNS  
SYVLNPTTGEVLFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLLI  
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 238-255

**N-glycosylation site.**

amino acids 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

**Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

## **FIGURE 45**

CAGCGCGTGGCCGGCGCCGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA  
GCGTGGCGAACAGGGCTCTGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT  
GGAGGCCGCCGAGCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG  
GCTCGTGCCACCCACCAAGTTCCAGTGCCGCACCAGTGGTTATGCGTGCCCTCACCTGG  
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC  
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA  
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA  
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCA  
CCCAGACTGTCCCGACTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCGGAAG  
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCC  
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTCGGAATGCCACATCCTC  
CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCTATGGGTTATTGCAGCTGCTGCC  
TCAGTGCAAGCCTGGTCACCGCCACCCCTCCTCTTTGTCCCTGGCTCCGAGCCAGGAGCGC  
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAAC  
CTCGCTGCCTGAGGACAAGCAACTGCCACCAACCGTCACTCACGCCCTGGCGTAGCCGGACA  
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGCACACCAGCCCTCAGAGACCTGAGTTCTT  
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC  
TGGACACTCCCTATGGAGATCCGGGAGCTAGGATGGGAACCTGCCACAGCCAGAAC  
GGGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGCCCTGTGCTTAAGAACACTCCCTGCTG  
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

1004

## **FIGURE 46**

MSGGWMAQVGAWRTGALGLALLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR  
TSGLCVPLTWRCRDLDCSDGSDEEECRIEPCQKGQCPPPPGLPCPCTGVSDCSGGTDKKL  
RNCsRLA CLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGGTNEILPEGDATTMGPPVT  
LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL  
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

### Signal sequence:

amino acids 1-30

### Transmembrane domain:

amino acids 230-246

N-glycosylation site.  
amino acids 126-130, 195-196

Casein kinase II phosphorylation site.  
amino acids 84-88, 140-144

N-myristoylation site.  
amino acids 3-9, 10-16, 26-27, 224-230, 230-236, 263-269

### Prokaryotic membrane lipoprotein lipid attachment site.

## amino acids 44-55

### Leucine zipper pattern.

## amino acids 17-39

## **FIGURE 47**

CCACCGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGAGCAGAGGTCGCGCACAGATGCGG  
GTTAGACTGGCGGGGGAGGAGGAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA  
CTCTTGCAGACTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG  
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG  
GCCGTGATCCTGTGGTTTAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGCGGGTT  
CGATGACCTCAAGTGTGCTGACCCGGCATTCCGAGAATGGCTTCAGGACCCCCAGCG  
GAGGGGTTTCTTGAGGCTCTGTAGCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG  
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCTAGGCTGGATCCAAGTGAA  
TAATTCCATCTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCTATA  
ACAAGACATATAGACATGGAGAGAACGCTAACATCACTTGTATGAAAGGATTCAAGATCCGG  
TACCCGACCTACACAATATGGTTCTATTATGTCGCGATGATGGAACGTGGAATAATCTGCC  
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTAATGGCTATGTAACATCTCTGAGC  
TCCAGACCTCCTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT  
GATGGGTCTGCGTATCTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCGGTG  
CCTTGCTCTGGAAGCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTCGTCT  
GCCACCCGGCCCTTGTGAGCGCTACAACCACGGAACGTGGTGAGTTACTGCGATCCT  
GGCTACAGCCTCACCAAGCGACTAACAGTACATCACCTGCCAGTATGGAGAGTGGTTCTTC  
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA  
CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGGTGCTGCTCGTCATC  
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGCTCCCCGGAG  
TTCCAGCAGTGACCTGACTTGTGGTAGACGGCGTCCCCGTATGCTCCGTCTATG  
ACGAAGCTGTGAGTGGCGCTTGAGTGCCTAGGCCCGGGTACATGGCCTCTGTGGGCCAG  
GGCTGCCCTTACCCGTGGACGACCAGAGCCCCCAGCATACCCGGCTCAGGGACACGGA  
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTGAGCTGCTCCAAA  
GTCTGTATTCACCTCCAGGTGCCAAGAGAGACCCACCTGCTGGACAACCTGACATA  
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCAGGCATCCATGCCACTGGGT  
GTTGTTCTAAGAAACTGATTGATTAAAAATTCCAAAGTGTCTGAAGTGTCTCTCAA  
ATACATGTTGATCTGTGGAGTTGATTCTTCTCTGGTTTAGACAAATGAAACAA  
AGCTCTGATCCTAAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTGATCAAGTC  
CTGTTCTTCTTGACACAGACTGATTAAAATTAAAAGNAAAAAA

## FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGVFFEGSVARFHQCQDGFKLKKGATKRLCLKHNGTLGWIPSDNSICVQEDCRI  
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS  
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP  
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT  
WPSTHETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSSDPDFVVVD  
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD'TDGPGESETCDS  
VSGSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVLFLRN

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 325-344

**N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

**Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

**N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

## **FIGURE 49**

CCACACGCGTCCGCTCCGCGCCCTCCCCCGCTCCCGTGCAGTCGGTCCGTGGTGGCCTAGAGA  
TGCTGCTGCCCGGGTGCAGTTGTCGCACGCCTCTGCCCGCCAGCCCGCTCCACCGCCGT  
AGCGCCCGAGTGTGGGGGGCCACCCGAGTCGGGCCATGAGGCCGGAAACCGCGCTACAGG  
CCGTGCTGCCGTGCTGGTGGCTGCCGGCCGCACGGGTCGCCGTGAGTGCC  
TCGGATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTTGTAA  
TAAAGTCATTTACTTCATGATACTTCTGAAGACTGAACACTTGAAGGAAAGCAAAGAACGCT  
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA  
AA~~TT~~TCATTGAAAACCTCTGCCATCTGATGGTACTTCTGGATTGGCTCAGGAGGCGTGA  
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATA  
CACAAATTAGGAAC~~T~~GGTATGTGGATGAGCCGTCTGCCAGCGAGGTCTCGTGGTCA  
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA  
CCGGTGCAACATGAAGAACAA~~TT~~CATTGCAAATATTCTGATGAGAAACCAGCAGTTCC  
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG  
GAAGAAGATGCCAAAAAAACATTAAAGAAAGTAGAGAACGCTGCCCTGAATCTGGCTACAT  
CCTAATCCCCAGCATTCCCCTCTCCTCCTCTGTGGTCACCACAGTTGTATGTTGGTT  
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCCTAGCACAAAGAACACACCAC  
TGGCCCTCTCCTCACCAAGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA  
AAGCGAAGCTGACTTAGCTGAGACCCGCCAGACCTGAAGAATATTCTCCGAGTGTGTT  
CGGGAGAAGCCACTCCGATGACATGTCTGTGACTATGACAACATGGCTGTGAACCCATCA  
GAAAGTGGTTGTGACTCTGGTGGAGAGTGGATTGTGACCAATGACATTATGA  
GTTCTCCCCAGACAAATGGGAGGAGTAAGGAGTCTGGATGGTGGAAAATGAAATATATG  
GTTATTAGGACATATAAAACTGAAACTGACAACAA~~T~~GGAAAAGAAATGATAAGCAAATC  
CTCTTATTTCTATAAGGAAAATACACAGAACAGTCTATGAACAAAGCTTAGATCAGGTCTGT  
GGATGAGCATGTGGTCCCCACGACCTCTGTGGACCCCCACGTTGGCTGTATCCTTAT  
CCCAGCCAGTCATCCAGCTGACCTTATGAGAACGGTACCTGCCAGGTCTGGCACATAGTA  
GAGTCTCAATAATGTCACTTGGTTGGTTGTATCTAACTTAAGGGACAGAGCTTACCTG  
GCAGTGATAAAAGATGGGCTGTGGAGCTGGAAAACCACCTCTGTTTCTGCTATACAG  
CAGCACATATTATCATACAGACAGAAAATCCAGAACATCTTCAAAGCCCACATATGGTAGCACAG  
GTTGGCCTGTGCATGGCAATTCTCATATCTGTTTTCAAAGAATAAAATCAAATAAAGA  
GCAGGAAAAAA

## FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGQTQRPCYKVIYFHDTSRRL  
NFEEAKEACRRDGGQLVSIESEDEQKLIKEFIENLLPSDGDFWIGLRRREEKQSNSTACQDL  
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPyMFQWNDDRCNMKNFICKY  
SDEKPAVPSREAEGEETELTPVLPETQEEDAKKTFKESREAALNLAYILIPSIPLLLLLV  
VTTVVVCWVWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL  
KNISFRVCSGEATPDDMSCDYDNMAVNPSSEGFTLVSVESGFVTNDIYEFSQDQMGRSKES  
GWVENEIYGY

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 117-121, 312-316

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 296-300

**Casein kinase II phosphorylation site.**

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327

**N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

## **FIGURE 51**

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGAAGGGCTGGATGTACGC  
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT  
GTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT  
GTTCAGCATGCGCTTGTGGACCCCAGTGGCGTCTGACCTCGCTGGCGTACTGCCTGCACC  
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTCGACCGCAGC  
CTGCTGAAGTTGAAAATGGTGCAGGTGCTGTTGACACGGGGCTCGGAGTCCTCTCAAGCC  
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC  
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATTCTCCTTACGACTCT  
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT  
GCAGCAAATGTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAAGACATTCCCTTC  
TTTCACCAACCTTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG  
GAGTCCACCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT  
CCACACTGATGAAGCAGATTAGAAGTCTTGTATCCAACTACCAAAGCTGCTGGAGCCTGA  
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG  
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGTAAAGTGGACTTCTCATCCTCCT  
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCAAAGCTGCCCATGCTGAAGAGATTG  
CACGGATGATCGAACAGAGAGACTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG  
GAAAGTCTTCAGATGGCAGTAGGCCATTCCCTCACATCCTAGAGAGCAACCTGCTGAAAGC  
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCGGCTCATGATG  
TGACCTTCATACCGCTTTAATGACCCCTGGGATTTTGACCACAAATGCCACCGTTGCT  
GTTGACCTGACCATGGAACCTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA  
TTACCAACGGGAAGGAGCAGGTGCCAGAGGTTGCCCTGATGGCTCTGCCGCTGGACATGT  
TCTTGAATGCCATGTCAGTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT  
TTAAAATAAGTGCCTTATACAATG

## **FIGURE 52**

MITGVFSMRLWTPGVVLTSAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR  
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL  
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNQEVFIRSTNIFRNLESTRCLLAGLFQCQKE  
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD  
FFILLDNVAAEQAHLPLSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLILES  
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW  
FVQLYYHGKEQVPRGCPDGLCP LDMLNAMS VYTLSPEKYHALCSQTQVM EVGNEE

**Signal sequence:**

amino acids 1-23

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

**Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

**Tyrosine kinase phosphorylation site.**

amino acids 280-288

**N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

**Amidation site.**

amino acids 216-220

**Leucine zipper pattern.**

amino acids 10-32

**Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

## **FIGURE 53**

CTCCTCTAACATACTTGCAGCTAAACTAAATATTGCTGCTGGGGACCTCCTCTAGCCT  
TAAATTCAAGCTCATCACCTCACCTGCCTGGTCATGGCTCTGCTATTCTCCTTGATCCTT  
GCCATTGCACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGC~~GG~~CTGGTGGGGGCCT  
CCACCGCTGTGAAGGGGGTGGAGGTGGAACAGAAAGGCCAGTGGGCACCGTGTGATG  
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGAGCTGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAGGTCTCATCCA  
ATCAGTCAGTTGCACAGGAACAGAACAGATACTTGGCTCAGTGTGAGCAAGAAGAAGTTATG  
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTTTCTCCCCA  
GTCCCAGAGGGTGTCAAGGCTGGCTGACGGCCCTGGCATTGCAAGGGACGCGTGGAAAGTGAA  
GCACCAAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGAAAGGTGG  
TGTGCCGGCAGCTGGATGTGGAGGGCTGTACTGACTCAAAACGCTGCAACAAGCATGCC  
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCTGCTCAGGACGAGAACCAACCTTCA  
GGATTGCCCTCTGGCCTGGGGAAAGAACACCTGCAACCATTGATGAAGACACGTGGTCG  
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGAACACCTCTGCTCTGGCGACTG  
GAGGTGCTGCACAAGGGGTATGGGCTCTGTGTGATGACAACACTGGGAGAAAAGGAGGA  
CCAGGTGGTATGCAAGCAACTGGCTGTGGAAAGTCCCTCTCCCTCCTCAGAGACCGGA  
AATGCTATGCCCTGGGTTGCCGCATCTGGCTGGATAATGTTGCTCAGGGAGGGAG  
CAGTCCCTGGAGCAGTGCACAGCACAGATTGGGGTTTCACGACTGCACCCACCAGGAAGA  
TGTGGCTGTCATCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA  
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGATGAACACTGATCT  
TCTTCTGCCCTGGACTGGACTTAACTTGGTGCCTGATTCTCAGGCCTCAGAGTTGG  
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGAACATACATCA  
CCACCTTCCTATGTCTCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTAT  
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACACATA  
CACCAATTGTCCTGTTCTGTGAAGAACTCTGACAAAATACAGATTGGTACTGAAAGAGA  
TTCTAGAGGAACGGAATTAAAGGATAAAATTCTGAATTGGTATGGGTTCTGAAATTG  
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTATTACAATAATAAGATAGCAC  
TATGTGTTCAAA

## **FIGURE 54**

MALLFSLILAICTRPGFLASPSGVRLVGGHLRCEGRVEEQKGQWGTVCDDGWDIKDVAVL  
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC  
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVQGTGWSLRAAKVVCRQLGCGRAVL  
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG  
GDNLCSRLEVHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIDL  
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

**Signal sequence:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

**N-myristoylation site.**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

**Amidation site.**

amino acids 196-200

**Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

## **FIGURE 55**

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTGACCTCGAC  
CCACCGCGTCCCGCGACCGCGTGGCGGACCGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG  
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCCTGGG  
CGTCTCGGCCCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAAGGCCTACCTGCGGAATGCTG  
TGGTGGTGATCACAGGCCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTCTATGCT  
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGCCCTAGAAGAGCTCATCAGAGA  
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTACTTGGTGACCTCGACC  
TCACAGACTCTGGGCCATAGTTGCAGCAGCTGAGATCCTGCAGTGCTTGCTATGTC  
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACACCAGTGG  
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCAGTTGCTCTAACGAAAGCACTCC  
TGCCCTCCATGATCAAGAGGGAGGAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG  
ATGAGCATTCTTTGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTG  
CTGTCTCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA  
TCCACACCAACCTCTGTAAATGCCATCACCAGGATGGATCTAGGTATGGAGTTATGGAC  
ACCACACAGCCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGG  
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTAAGCAGGAGGATGTTCTGCTGCTGG  
CTCTGGCTCCTGGCTCTTCAGCCTCATGGCCTCCAGGGCAGAAAAGAGCGGAAATCC  
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGGGCAGAGAACGACTCTTAGGCTTGC  
TTACTCTACAAGGGACAGTTGCATTGAGACTTTAATGGAGATTGCTCTACAAGTGG  
AAAGACTGAAGAAACACATCTGTGCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA  
AGCTTCTCCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT  
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAGGGCGCCGCGACTCTAG  
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTGTTATTGCAGCTTATAATGGTTAC

## **FIGURE 56**

MDFITSTAILPLLFGCLGVFGLFRLQQWVRGKAYLRNAVVIITGATSGLGKECAKVFYAAGA  
KLVLICRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI  
VAAAEEILQCFGYVDIL  
VNNAGISYRGTIMDTTVVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI  
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTT  
AQGRSPVEVAQDVLAAGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKS KNS

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 104-120, 278-292

**N-glycosylation site.**

amino acids 228-232

**Glycosaminoglycan attachment site.**

amino acids 47-51

**Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

**Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

**N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

**Amidation site.**

amino acids 265-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17

## **FIGURE 57**

CCACCGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTAGAGTGGTAAAAAA  
AAAAAAAAACACACCAACGCTCGCAGCCACAAAAGGG**GATGAA**ATTCTCTGGACATCCTC  
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTATTCTAA  
GAGGAGAAAATCAGTCACCGGCAGAACATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA  
GA**CTGACTGCCTATGA**ATTGCTAAACTAAAGCAAGCAGTGGTCTCTGGATATAAATAAG  
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTACACTTGT  
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG  
GAGATGTTAGTATTAGTAAATAATGCTGGTAGTCTATACATCAGATTGTTGCTACA  
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGACACATTCTGGACTACAAA  
GGCATTCTCCTGCAATGACGAAGAATAACCATTGCCATATTGTCAGTGGCTCGGCAG  
CTGGACATGTCGCGTCCCCTCTTACTGGCTACTGTTCAAGCAAGTTGCTGTTGGA  
TTTCATAAAACTTGACAGATGAACTGGCTGCCTACAAATACTGGAGTC  
AAAACAAACATG  
TCTGTGCTTAATTGTAACACTGGCTTCATCAAAATCCAAGTACAAGTTGGACCCA  
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGATTCTGACTGAGCAGAAGATG  
ATTTTATTCCATCTTCTATAGCTTTTAACAACATTGAAAGGATCCTCCTGAGCGTTT  
CCTGGCAGTTTAAAACGAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA  
AAGCGCA**AT**AAGCACCTAGTTCTGAAAATGATTACCAAGGTTAGGTTGATGTCATCTA  
ATAGTGCAGAATTAAATGTTGAACCTCTGTTTTCTAATTATCCCCATTCTCAATA  
TCATTTTGAGGCTTGGCAGTCTCATTACTACCACTGTTCTTAGCCAAAAGCTGATT  
ACATATGATATAAACAGAGAAACCTTAGAGGTGACTTAAGGAAAATGAAGAAAAGAA  
CCAAAATGACTTTATTAAAATAATTCCAAGATTATTGTTGGCTCACCTGAAGGCTTGCAA  
AATTGTA**CCATAACCGTT**TTAACATATATTATTGATTGACTTAAATTGTTG  
ATAATTGTTCTTTCTGTTCTACATAAAATCAGAAACTCAAGCTCTCAAATAAAA  
TGAAGGACTATCTAGTGGTATTCAACATGAATATCATGAACACTCTCAATGGTAGGTT  
ATCCTACCCATTGCCACTCTGTTCTGAGAGATACCTCACATTCAATGCCAAACATTCT  
GCACAGGGAAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTAAAG  
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAAA  
AA  
AA

## **FIGURE 58**

MKFLLDILLLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGI  
GRLTAYEFAKLKSK  
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDV  
SILVNNAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTKAFLPAMTKNNHGHIVTVASAAGH  
VSVPFLLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTS  
LGPTLEPEEVVNRLMH  
GILTEQKMFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

### Signal sequence:

amino acids 1-19

## cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

### Casein kinase II phosphorylation site

amino acids 52-56 95-99 198-203 267-271

### N-myristoylation site

amino acids 43-49 72-78 122-128 210-216

## **FIGURE 59**

CCACCGCGTCCGGACCGTGGGCGACTAGTTAGATCGCGAGCGGCCGCCGCGCTC  
AGGGAGGAGCACCAGCTGCGCCGCACCCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTG  
TTTCGCTGGCCTGTTGATGCCTGGCCCTGTGATGGGCTGTTCGCTCCCTATACAGAAGT  
GTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTCTCACCCCTTACATTGAAGC  
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGGTCGGCCCTTCCCAGGACTGAACATGA  
AGAGTTATGCCGGCTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTCTGGTTC  
TTCCCAGCTCAGATACAGCCAGAAGATGCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG  
AGGTTCATCCATGTTGGACTCTTGTGGAACATGGCCCTATGTTGTACACAAGTAACATGA  
CCTTGCCTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA  
GTGGGCACAGGCTTCAGTTACTGATGATACCCACGGATATGCAGTCATGAGGACGATGT  
AGCACGGGATTATACAGTGCACTAATTCAAGTTTCAGATATTCTGAATAATAAAAATA  
ATGACTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC  
ATCCATTCCCTCAACCCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA  
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGCAGAATTCTGTACCAAATTGGCT  
TGTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC  
AGGAAGCAGAACTGGTTGAGGCCTTGAAATACTGGATAAAACTACTAGATGGCAGTTAAC  
AAAGTGTACCTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCCTG  
GCACGGAACCTGAGGAATCAGCTTACTATGAAATTGGTCACTCCCAGAGGTGAGACAA  
GCCATCCACGTGGGAATCAGACTTTAATGATGGAACATAGTTGAAAGTACTTGCAGA  
AGATACAGTACAGTCAGTTAACCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA  
TCTACAATGCCAACGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTGATGGC  
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAGTTGGAAGATCTTAA  
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATC  
GAGGTGGAGGACATATTTCACCTATGACCAGCCTCTGAGAGCTTGACATGATTAATCGA  
TTCATTATGGAAAAGGATGGATCCATTGTTGATAAAACTACCTCCAAAAGAGAACAT  
CAGAGGTTTCATTGCTGAAAAGAAAATCGTAAAACAGAAAATGTCATAGGAATAAAAAAA  
TTATCTTTCATATCTGCAAGATTTCATCAATAAAAATTATCCTGAAACAAGTGAGC  
TTTGTTTTGGGGGAGATGTTACTACAAATTAAACATGAGTACATGAGTAAGAATTACA  
TTATTTAACTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAAGATGTATAATGA  
AATTAAAGGGCTTGAATAGGAAGTTTAATTCTCTAAGAGTAAGTGAAGGAAAGTGCAGTTG  
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT  
GTTGGAAATATTATGGATAAGAATAGCTCAATTATCCCAAATAATGGATGAAGCTATAA  
TAGTTTGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAACATTCTTGAAATA  
AAAATATTATATAAAAGTAAAAAA

## **FIGURE 60**

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPPKGDSGQPLFLTPYIEAGKIQKGREL  
VGPFPGNMKSYAGFLTVNKTYNSNLFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPYVVTTSNMTLRDRDFPWTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF  
FQIFPEYKNNDFYVTGESYAGKYVPAIAHЛИHSLNPVREVKINLNGIAIGDGYSDPESIIGG  
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFFEILDKLLDGDLTSDPSYFQNV  
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGQTFNDGTIVEKYLREDTVQSVKPWLT  
EIMNNYKVLIYNGQLDIIVAALTERSLMGMDWKGSQEYKKAEEKVWKIFKSDSEVAGYIRQ  
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

**Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428

**Tyrosine kinase phosphorylation site.**

amino acids 423-432

**N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

**Serine carboxypeptidases, serine active site.**

amino acids 200-208

**Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

## **FIGURE 61**

CGAGGGCTTCCGGCTCGGAATGGCACATGTGGGAATCCAGTCTGTTGGCTACAACATT  
TTTCCCTTCTAACAGTCTAACAGCTTCTAACAGCTAGTGATCAGGGTTCTCTT  
GCTGGAGAAGAAAGGGTGGAGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAAGCTCCTT  
CCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGGGAGTGAGGTGATGGAAG  
TCTAAAATAGGAAGGAATTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC  
CTGGGGAGGGCTGCTAACAAAGCTTCAAAAAACAGGAGCGACTCCACTGGGCTGGGAT  
AAGACGTGCCGGTAGGATAGGGAAAGACTGGGTTAGTCCTAACATCAAATTGACTGGCTGGG  
TGAACCTCAACAGCCTTTAACCTCTGGAGATGAAAACGATGGCTTAAGGGCCAGAAA  
TAGAGATGCTTGTAAAATTTAAAAAAAGCAAGTATTATAGCATAAAGGCTAGA  
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAACAGAGGGAGAAAGTATGTTAAAATA  
GAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAACCAAGGATGGGACCTGGT  
AGGCCAGCCTCTTGCTCCTCCGGAAATTATTTGGTCTGACCACTCTGCCTTGTGTTT  
GCAGAATCATGTGAGGGCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT  
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGCCCTGGAGGTGG  
ACAGCCGCTCTGTGGTCTGCTCTCAGTGGCTGGGTGCTGGCCCCCAGCAGCCGGC  
ATGCCTCAGTTCAGCACCTCCACTCTGAGAATCGTACTGGACCTCAACCAACTGACCCT  
CCACCAAGGGACGGGGCGTCTATGTGGGGCATCAACCGGTCTATAAGCTGACAGGCA  
ACCTGACCATCCAGGTGGCTCATAGACAGGGCAGAAGAGGACAACAAGTCTCGTACCCG  
CCCCTCATCGTGCAGCCCTGCAGCGAAGTGTCTACCCCTACCAACAATGTCAACAAAGCTGCT  
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGGAGCCTCTACCAAGGGGTCTGCA  
AGCTGCTGCCGTGGATGACCTTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC  
CTGTCCAGTGTCAACAAAGACGGCACCATGTACGGGTGATTGTGCGCTTGAGGGTGAGGA  
TGGCAAGCTCTCATCGGCACGGCTGTGGATGGAAGCAGGATTACTTCCGACCCCTGTCCA  
GCCGGAAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT  
TTTGTCTCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCACTTGACAT  
CTTCTACATCTACGGCTTGCTAGTGGGGCTTGTCTACTTCTCACTGTCCAGCCGAGA  
CCCCTGAGGGTGTGGCATCAACTCCGCTGGAGACCTCTACACCTCACGCATCGTGC  
CTCTGCAAGGATGACCCAAGTCCACTCATACGTGCTCCCTGCCCTGGCTGCACCCGGG  
CGGGGTGGAATACCGCCCTCTGCAGGCTGCTTACCTGGCCAAGCCTGGGACTCACTGGCC  
AGGCCTCAATATCACCAGCCAGGACGATGTACTCTTGCCATCTCTCAAAGGGCAGAAG  
CAGTATCACCAACCCGCCGATGACTCTGCCCTGTGCTGCCCTATCGGGCCATCAACTT  
GCAGATCAAGGAGCGCCTGCAGTCCTGCTACCAAGGGCGAGGGCAACCTGGAGCTCAACTGGC  
TGCTGGGAAGGACGTCAGTGCACGAAGGCGCTGTCCCCATCGATGATAACTCTGTGGA  
CTGGACATCAACCAGGCCCTGGGAGGCTAACCTCAGTGGAGGGCTGACCCCTGTACACCAC  
CAGCAGGGACCGCATGACCTCTGTGCCCTACGTTACAACGGCTACAGCGTGGTTTTG  
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAAGAGTCTATGAGTTCAGATGCTCAAATGCC  
ATTCACCTCCTCAGCAAAGAGTCCCTGTGGAGGTAGCTATTGGTGGAGATTAACTATAG  
GCAACTTTATTTCTGGGAACAAAGGTGAAATGGGGAGGTAAGAAGGGTTAATTTGTG  
ACTTAGCTTAGCTACTCCCTCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA  
TTCAATATTCCTCAAACTTAAGAAAAACTTAAAGAAGGTACATCTGCAAAAGCAAA

## FIGURE 62

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP  
RALEVDSRSVVLLSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV  
YKLTGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLLACGSL  
YQGVCKLLRLDDLFLILVEPSHKKEHYLSSVNKTGTMGVIVRSEGEDGKLFIGTAVDGKQDY  
FPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKIIPSDTLALVSHFDIFYIYGFASGGFVYFL  
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP  
GDSLQAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAINLQIKERLQSCYQGEGN  
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG  
YSVVFGTKSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

**Signal sequence:**

amino acids 1-32

**Transmembrane domain:**

amino acids 71-87

**N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

**Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534

**N-myristylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

## **FIGURE 63**

AGGCTCCCGCGCGCGGCTGAGTGGACTGGAGTGGAAACCGGGTCCCGCGCTTAGAGAACACCGCGATGACCA  
CGTGGAGCCTCCGGCGGAGGCCGGCCCGACCGCTGGACTCCCTGCTGCTGGTCTTGGGCTTCCCTGGTCTCC  
GCAGGCTGGACTGGAGCACCCCTGGTCCCTGCGGCTCCGCATCGACAGCTGGGCTGCAGGCCAAGGGCTGGA  
ACTTCATGCTGGAGGATTCCACCTCTGGATCTCGGGGCTCCATCCACTATTCCTGCTGCCAGGGACTACT  
GGAGGGACCGCTGCTGAAGATGAAGGCCTGGCTTGAAACACCCACCACCTATGTTCCGTGAAACCTGCATG  
AGCCAGAAAGAGGCAAATTGACTTCTCTGGAACCTGGACCTGGAGGCTTCGTCCTGATGGCCAGAGATCG  
GGCTGTGGTGAATTCTGCTCCAGGCCCTACATCTGCACTGAGATGGACCTGGGGCTTGCCAGCTGGCTAC  
TCCAAGACCCCTGGCATGAGGCTGAGGACAACCTACAAGGGCTCACCGAAGCAGTGGACCTTATTGACCAC  
TGATGTCAGGGTGGCCACTCCAGTACAAGCGTGGGGACCTATCATTGCGTGCAAGTGGAGAATGAATATG  
GTTCTATAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGTGAACTGC  
TCCTGACTTCAGACAACAAAGGATGGCTGAGCAAGGGATTGTCCAGGGACTCTGGCACCATCAACTTGCAGT  
CAACACACGAGCTGCAGCTACTGACCACCTTCTCTAACGTCCAGGGACTCAGGCCAAGATGGTATGGAGT  
ACTGGACGGGGTGGTTGACTCGTGGGAGGGCCCTCACAAATATCTGGATTCTCTGAGGTTTTGAAAACCGTGT  
CTGCCATTGTGGACGCCGCTCTCCATCAACCTCTACATGTTCCACGGAGGGCACCAACTTGGCTTCATGAATG  
GAGCCATGCACTTCATGACTACAAGTCAGATGTCACCGACTATGACTATGATGCTGTGACAGAACGCCGCG  
ATTACACGGCAAGTACATGAAGACTTCGAGACTTCTGGCTCCATCTCAGGCATCCCTCCCTCCCCCACCTG  
ACCTTCTTCCAAGATGCGTATGAGCCCTAACGCCAGTCTGTACCTGCTCTGTGGGACGCCCTCAAGTACC  
TGGGGAGCCAATCAAGTCTGAAAAGCCATCAACATGGAGAACCTGCCAGTCATGGGGAAATGGACAGTCCT  
TCGGGTACATTCTATGAGACCAGCATCACCTCGTCTGGCATCTCAGTGGCACGTGATGTCAGGGCAGG  
TGTTGTGAACACAGTATCCATAGGATTCTGGACTACAAGACAACGAAGATGCTGTCCCCCTGATCCAGGGTT  
ACACCGTGTGAGGATCTGGTGGAGAATCGTGGGCGACTCAACTATGGGAGAATATTGATGACCAAGCGCAAAG  
GCTTAATTGGAAATCTATCTGAATGATTCAACCCCTGAAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA  
GCTTCTTCAGAGGTTGCCCTGGACAAATGGNTTCCCTCCAGAAACACCCACATTACCTGCTTCTTCTTGG  
GTAGCTTGTCCATCAGCTCCACGCCCTGTGACACCTTCTGAAGCTGGAGGGCTGGAGAAGGGGGTTGTATTCA  
TCAATGCCAGAACCTGGACGTTACTGGAACATTGGACCCAGAACAGCCTTACCTCCAGGTCCCTGGTGA  
GCAGCGGAATCAACCAGGTACGTTTGAGGAGACGATGGCGGCCCTGCATTACAGTCAGGAAACCCCCC  
ACCTGGCAGGAACCAGTACATTAAGTGAGCGTGGCACCCCTCTGCTGGTGCCTGGGAGACTGCCGCTC  
CTCTTGACCTGAAGCCTGGCTGCTGCCACCCCTCACTGCAAAAGCATCCTTAAGTAGCAACCTCAGGG  
ACTGGGGCTACAGTCTGCCCTGCTCAGCTCAAACCTTAAGCCTGCAGGAAAGGTGGATGGCTCTGGGCC  
TGGCTTTGTTGATGTCAGGCTTCTCAAGGCCCTGCTCTGTGCGCAGGCTGTCGGCTGTCTAGGGTGGAGC  
AGCTAATCAGATGCCCAAGCCTTGGCCCTCAAGAAAAGTGTGAAACAGTGCCTTGCACCGGACGTACAGCCC  
TGCAGCATCTGCTGGACTCAGCGTGTCTGGTGTCAACAGTGTAGAGGGTGGGAAGGGGTGTCACCTGAGCTGACTTTGTT  
TTTATCCCCGAAATCCTGGGTGTGTCACAGTGTAGAGGGTGGGAAGGGGTGTCACCTGAGCTGACTTTGTT  
CTTCCCTCACACCTCTGAGCCTTCTGGGATTCTGGAAAGGAACCTGGCGTGAGAAAATGTGACTTCCCCCTT  
TCCCTCCCACTCGCTGCTTCCACAGGTGACAGGCTGGAGAAACAGAAATCCTCACCCCTGCGTCTTCC  
CAAGTTAGCAGGTGTCTGGTGTCACTGAGTGGAGGACATGTGAGTCCCTGGCAGAACGCCATGGCCCATGTCTGCA  
CATCCAGGGAGGAGGACAGAACAGGCCAGCTCACATGTGAGTCCCTGGCAGAACGCCATGGCCCATGTCTGCAACATCC  
AGGGAGGAGGACAGAACAGGCCAGCTCACATGTGAGTCCCTGGCAGAACGCCATGGCCCATGTCTGCAACATCCAGGG  
GGAGGACAGAACAGGCCAGCTCACATGTGAGTCCCTGGCAGAACGCCATGGCCCATGTCTGCAACATCCAGGGAGGAGG  
ACAGAACAGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCACGCCGAACAGCAGGGGAGGAGCAGGCCATGGCCCTTC  
GAAGTGTGTCCAAGTCCGATTGAGCCTGTTCTGGGGCCAGCCAAACACCTGGCTTGGCTACTGTCTGA  
GTTGCAGTAAAGCTATAACCTGAATCACAA

## **FIGURE 64**

MTTWSLRRR PART LGLLL VV LGFLV LRR LDW STLVPL RL RHQ LQL QAK GWN FM LED STFW  
I FGG SI HYFRV PREY WRD RLL KMK ACGL NT LTT YPV WNL HEP ERG KF DF SGN LD LEAF VL MA  
AE IGL WVL R PGP YIC SEM DLG GLP SWL LD PG MRL RTT YKG FTE A VD LY FDH LMS RVV PLO  
YKR GGPI IAV QVENEY GS YNK DPA YMP YV KKA LED RG IVE LLL TSDN KDG LSK GIV QGV LAT  
INL QSTH EQL LTT F LFNV QGT QPK MVME YWT GWF DSW GGPH NILD S SEV LKT VSA IVD AGS  
S IN LYMF HGGT NFG FMNGA MHF HDY KSD VTSY DYDA VL TEA GDY TAK YM KLR DFF GSI SGIP  
L PPPP D L L P KMP YEPL TPV LYLS LWD ALK YLGE PIK SEK P INMEN LPV NGNG QSF GYI LY  
TSIT SSG ILS GHV HD RGQV FVNT VSI GFL DYKTT KIA VPLI QGY TVL RIL VENR GRV NYGEN  
ID DQR KGL IGL NLYL ND SPL K NFR IY S LDM KKS F QRF GLD KWX SLP ETPT LPAFF LG SLS IS  
S TPC DTF LKLEG WEG VV FING QNL GRY WNI GPQ KTL YLPG PWL SSG INQ VIV FEET MAG PA  
LQFTET PHL GRN QYIK

Signal sequence:  
amino acids 1-27

Casein kinase II phosphorylation site.  
amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristylation site.  
amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,  
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

## **FIGURE 65**

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCAGGAC  
CTGGTGAGGGTTCTACTTGGCCTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAGGG  
GGAGCAAAGCCGGCTGGCCGAGGCCAGGACCTCCATCTCCAATGTTGGAGGAATC  
CGACACGTGACGGTCTGTCGCGCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC  
AAGAAGCTGTCCTGCCTCGTCCCTGCTGCTGCCGCTAGCCTGACGCTACTGCTGCCCA  
GGCAGACACTCGGTGTTGTAGTGGATAGGGGTATGACCGGTTCTCCTAGACGGGGCC  
CGTTCGGCTATGTGTCTGGCAGCCTGCACTACTTTCGGTACCGGGTGGCTTGGCCGAC  
CGGCTTTGAAGATGCGATGGAGCGGCCAACGCCATACAGTTATGTGCCCTGGAACTA  
CCACGAGCCACAGCCTGGGGTCTATAACTTAATGGCAGCCGGACCTCATTGCCTTCTGA  
ATGAGGCAGCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAG  
TGGGAGATGGGGGTCTCCCATCTGGTGTGAAACCTGAAATTCACTAAGAACCTC  
AGATCCAGACTCCTTGCCGAGTGGACTCTGGTTCAAGGTCTGCTGCCAAGATATATC  
CATGGCTTATACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC  
TACAGAGCCTGTGACTTCAGCTACATGAGGCACCTGGCTGGCTTCCGTGACTGCTAGG  
AGAAAAGATCTGCTCTCACACAGATGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG  
GACTCTATACCACTGTAGATTGGCCAGCTGACAACATGACCAAAATTTACCCCTGCTT  
CGGAAGTATGAACCCATGGCCATTGGTAAACTCTGAGTAACACAGGCTGGCTGGATT  
CTGGGCCAGAATCACTCCACACGGTCTGTCAGCTGTAACCAAAGGACTAGAGAACATGC  
TCAAGTTGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG  
AATGGTGCCTGATAAGAAGGGACGCTTCCCTCGATTACTACCAGCTATGACTATGATGCACC  
TATATCTGAAGCAGGGACCCACACCTAACGTTTGCTCTTGAGATGTCATCAGCAAGT  
TCCAGGAAGTCCCTTGGACCTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG  
ACTCTGCACCTGGTGGCATTACTGGCTTCTAGACTTGCTTGGCCCCGTGGCCCAT  
TCATTCAATCTGCCAATGACCTTGAGGCTGTCAAGCAGGACCATGGCTCATGTTGTACC  
GAACCTATATGACCCATACCATTGGAGCCAACACCATTGGTGCCTAACATGGAGTC  
CATGACCGTGCCTATGTGATGGGGATGGGTGTTCCAGGGTGTGGAGCGAAATATGAG  
AGACAAACTATTTGACGGGAAACTGGGTCAAACACTGGGATATCTGGTGGAGAACATGG  
GGAGGCTCAGCTTGGGCTAACAGCAGTGACTTCAGGGCTGTGAAGCCACCAATTCTG  
GGGCAAACAATCTTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTGTGAAGTG  
GTGGTTCCCTCCAGTTGCCAAATGGCCATATCCTCAAGCTCCCTCTGGCCCCACATTCT  
ACTCCAAAACATTCCAATTAGGCTCAGTGGGACACATTCTATATCTACCTGGATGG  
ACCAAGGGCAAGTCTGATCAATGGTTAACCTGGCCGTACTGGACAAAGCAGGGGCC  
ACAACAGACCCCTACGTGCCAAGATTCCCTGCTGTTCTAGGGGAGCCCTAACAAAATTA  
CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTGGATAAGCCTATC  
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG  
TGCCTCTGAACCAATGGAGTTAAGTGGGCACTGAAAGGTAGGCCGGCATGGTGGCTCATGC  
CTGTAATCCAGCACTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA  
CCAGCCTGGCCAACATGGTAAACCCGCTCCACTAAAAATACAAAATTAGCCGGCGTG  
ATGGTGGCACCTCTAACCTCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC  
AGGAGGGAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACCTCAGCCTGGCTGACAGTGA  
GACACTCCATCTCAAAAAAAAAAA

## **FIGURE 66**

MAPKKLSCLRSLLLPLSLTLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL  
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE  
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF  
TLLRKYEPHGPLVNSEYYTGWLWQNHSTRSAVTKGLENMLKLGASVNMYMFHGGTNF  
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPGLPPSPKML  
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMHTIFEPTFWVPN  
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRSLFGSNSSDFKGLLKP  
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL  
PGWTKGQVWINGFNLGRYWTQOGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD  
KPILNSTSTLHRTHINSLSAADTLSASEPMELSGH

09027580300  
T90700

**Signal sequence:**

amino acids 1-27

**N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

**Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

**Tyrosine kinase phosphorylation site.**

amino acids 191-198

**N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

## **FIGURE 67**

GCTTGAAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTGAGTGC  
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT  
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAGGATACCTTGAAGGAATATT  
CTTCGAAAAAGTCAGAGAAGAGAGCAGTTAGTGACATTCCAGATGTCAAAAACGATTT  
GCGTTCCCTTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT  
CTTGTCAAGAGTTAGTGAAAATAACTTAGGAAATTAGTTGAACCATGAGTGGACATTG  
AAAAACTCAGGCAGCACATTCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG  
CTGTCGGGGGTGCCGATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC  
AATTCCAGAAGCTAAAATTCTGCTAACAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC  
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTAGCTTCTCGCGATCACTTGAGA  
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCTGGGTGTATTGCTCAAAA  
CCTTCGAGAGTTGACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG  
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCACGTGAAGAGCAATTGACCAAAGTT  
CCCTCCAACATTACAGATGTGGCTCCACATCTAACAAAGTTAGTCATTATAATGACGGCAC  
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCCAGA  
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAACAGGAACACTGGAT  
TTAAAGTCCAATAACATTGCACAATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT  
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTCTATTACCCATGTCA  
AAAACTTGGAGTCACTTATTCTCTAACACAAGCTCGAACCTTACCACTGGCAGTATT  
AGTTACAGAAAACTCAGATGCTTAGATGTGAGCTACAACAAACATTCAATGATTCCAATAGA  
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAACAAAGTGGACATTCTGC  
CAAAACAATTGTTAAATGCATAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC  
TCACCTCCAGAGAAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG  
CTTGGACCGCCTGCCAGCCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTTGTG  
TGGAAGATCACCTTTGATAACCTGCCACTCGAACGTCAAAGAGGCATTGAATCAAGACATA  
AATATTCCCTTGCAAATGGATTTAAACTAAGATAATATGACAGTGTGAGGAAAC  
AACTCCTAGATTGCAAGTGCTACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG  
ATACATCTTTAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT  
GTTCAATGTTGAGGGTTTAAGTCATTCAACATTTCAATCATTGTTTTCTTTGGGG  
AAAGGGAAGGAAAATTATAATCACTAATCTGGTTCTTTAAATTGTTGTAACCTGGAT  
GCTGCCGCTACTGAATGTTACAAATTGCTGCCTGCTAAAGTAAATGATTAAATTGACATT  
TTCTTACTAAAAAAAAAAAAAA

## FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL  
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLQRQHISRNAQDKQELHLFMLSG  
VPDAVFDLTDLDVLKLELIPAKEKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH  
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMIGLESLRELRLKILHVKSNLTKVPSN  
ITDVAPHLTKLVIHNDGKLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS  
NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ  
KLRCLDVSYNNISMPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP  
EKVGQLSQLTQLELKGNCNDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP  
FANGI

**Signal sequence:**

█ amino acids 1-20

█ **N-glycosylation site.**

█ amino acids 241-245, 248-252, 383-387

█ **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

█ amino acids 326-330

█ **Casein kinase II phosphorylation site.**

█ amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

**Tyrosine kinase phosphorylation site.**

█ amino acids 349-355, 375-381

**N-myristoylation site.**

█ amino acids 78-84, 124-130, 212-218, 392-398

## FIGURE 69

CCACACGCGTCCGGCCTCTCTGGACTTGCATTCCATTGACAAACTGACTTTTTATTTCT  
TTTTTTCCATCTCTGGGCCAGCTGGGATCCTAGGCCGCCCTGGGAAGACATTGTGTTTACACACATAAGGAT  
CTGTGTTGGGTTTCTTCTTCCTCCCTGACATTGGCATTGCTTAGGTACATCGAAGTCTTGACCTCCACAGTATTGTC  
GCTCAGTGCCTGCTTGCACTTATGCCTAGGTACATCGAAGTCTTGACCTCCACAGTATTGCTGTC  
ATCGCTGGTGGTATCCTGGCGCTGCTCCTGCTGATAGTTGTCGTCTGTCTTACTTCAAATACACAAAC  
GCGCTAAAAGCTGCAAAGAACCTGAAGCTGTTGCTGAAAAATACAACCCAGACAAGGTGTGGTGGGCCAAG  
AACAGCCAGGCCAAACCATGGCACCGAGTCTGCTGCTGCCCTGCACTGCTGTAAGGATATAGAATGTGTGCC  
AGTTTGATTCCCTGCCACCTTGCTGCTTGCGACATAATGAGGGCTCTGAGTTAGGAAGGCTCCCTCTCAA  
GCAGAGCCCTGAAGACTTCAATGATGCAATGAGGCCACCTGTTGATGTCAGGCACAGAAGAAAGGCACAG  
CTCCCCATCAGTTCATGAAAATAACTCAGTGCCTGCTGGGAAACAGCTGCTGGAGATCCCTACAGAGAGCTTC  
CACTGGGGCAACCCCTTCAGGAAGGAGTGGGGAGAGAGAACCCCTACTGTTGGGAATGCTGATAAAACAGTCA  
CACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCGTGGCTGAACTGACGTTTCCCTGGAGGTGTCCAGAAA  
GCTGATGTAACACAGAGCTATAAAAGCTGTCGGCTTAAGGCTGCCAGGCCCTGCCAAAATGGAGCTTGT  
AGAAGGCTCATGCCATTGACCCCTTAATTCTCCTGTTGGCGAGCTGACAATGGGGAGGCTGAAGGCAAT  
GCAAGCTGCACAGTCAGTCTAGGGGTGCAAATATGGCAGAGACCCACAAGGCATGATCTGCAACTCAATCCC  
AGTGAGAACTGCACCTGGACAATAGAAAGACCAAGAAAACAGCATCAGAATTATCTTCTATGTCCAGTT  
GATCCAGATGGAAGCTGTGAAAAGTCAAAGCTTGTGAGGAACTCCAGCAATGGGCTCTGCTAGGG  
CAAGTCTGCAGTAAAAGCACTATGTTCTGTATTGAAATCATCATCCAGTACATTGACGTTCAAATAGTTACT  
GAECTCAGCAAGAATTCAAAGAACTGTCTTGCTTCTACTACTTCTCTCTAACTCTCTATTCCAAACTGT  
GGCGGTTACCTGGATACCTTGGAAAGGATCCTCACCGCCCAATTACCCAAAGCCGCATCCTGAGCTGGTTAT  
TGTGTTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTCAAAGAGATTTCCTAGAAATAGAC  
AAACAGTGCACATTGATTCTTGCATCTATGATGGCCCTCCACCAACTCTGGCTGATTGGACAAGTCTGT  
GGCCGTGTGACTCCCACCTCGAATCGTCATCAAACCTCTGACTGTCGTGTTGCTACAGATTATGCCAATTCT  
TACCGGGGATTTCTGCTCCTACACCTCAATTATGCAAGAAACATCAACACTACATCTTAACTTGCCT  
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGTTAACTCTAATGGAATAACTTGCAACTAAA  
GACCCAATTGCAAGACCAAAATTCAAATGTTGGAATTCTGTCCTCTTAATGGATGTGGTACAATCAGA  
AAGGAGAAGTCAGTCATTACACCAATAATCACCTTCTGATCCTCTCAACTTCTGAAAGTGTACCC  
CGTCAGAAACAACTCCAGATTATTGTAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATAACATAACA  
GAAGATGATGTAATCAAAGTCAAATGCACTGGGAAATATAACACCAGCATGGCTTTGAAATCCAATTCA  
TTTGGAAAAGACTATACTTGAATCACCATATTATGTTGAGGTTGAAACCAACTCTTGTCAAGTTAGTCTGCAC  
ACCTCAGATCAAATTGTTGGTCTTGTACCTGTAGAGCCTCTCCACCTCTGACTTTGCATCTCCAAACC  
TACGACCTAATCAAGAGTGGATGTAGTCAGATGAAACTTGTAAAGGTGTATCCCTTATTGGACACTATGGGAGA  
TTCCAGTTAATGCCTTAAATTCTGAGAAGTATGAGCTGTGTATCTGCACTGTAAGTTGATATGTGAT  
AGCAGTGCACCAAGTCTCGCTGCAATCAAGGTTGTTCTCAGAAGCAAACAGAGACATTCTCATATAATGG  
AAAACAGATTCCATCATAGGACCCATTGCTGAAAAGGGATGCAAGTGCAGTGGCAATTCAAGGATTTCAGCAT  
GAAACACATGCCAAGAAACTCCAAACAGCCCTTCAACAGTGTGCACTGTTCTCATGGTTCTAGCTCTG  
AATGTGGTACTGTAGCGACAATCACAGTGAGGCATTGAAATCAACGGGAGACTACAAATACCAGAAGCTG  
CAGAACTATTAACTAACAGGTCCAACCTAAGTGAGACATGTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT  
GGCTACACATATTGAATAATGAGGAAGGGCCTGAAAGTGACACACAGGCCTGCATGAAAAAAA

## **FIGURE 70**

MELVRLMPPTLLILSCLAEATMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI  
ERPENKSIRIIIFSYVQLDPGSCESENIVFDGTSSNGPLLQVCSKNDYVPVFESSSTLT  
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV  
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSNTSGLIGQVCRVTPTFESSNSLTVVLS  
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP  
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGNST  
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTIILESPYYVQLNQTLFVQVSLHTSDPN  
LVVFLDTCRASPTDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNFKFLRSMSSVYL  
QCKVLICDSSDHQSRCNQGCVRSRSKRDISSYWKTDIIGPIRLKRDRSASGNSGFQHETHA  
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

**Signal sequence:**

amino acids 1-24

**Transmembrane domain:**

amino acids 571-586

**N-glycosylation site.**

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

**Casein kinase II phosphorylation site.**

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560

**Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

**N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 71**

GACGGAAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG  
GGACATGCGGCCCCCAGGAGCTCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGC  
TGCTGCCGCCGCCGTGCCCTGCCACAGCGCCACGCCGCTCGACCCCACCTGGGAGTCC  
CTGGACGCCGCCAGCTGCCCGCGTGGTTGACCAGGCAAGTCGGCATCTCATCCACTG  
GGGAGTGTTCGCGCCAGCTCGGTAGCGAGTGGTCTGGGGTATTGGCAAAAGGAAA  
AGATACCGAAGTATGTGAATTATGAAAGATAATTACCCCTCTAGTTCAAATATGAAGAT  
TTGGACCACTATTACAGCAAAATTTTAATGCCAACAGTGGCAGATATTTCAGGC  
CTCTGGTGCAAATACATTGTCTTAACCTCAAACATCATGAAGGCTTACCTGGGGGT  
CAGAATATTGTGGAACGTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAGGAA  
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTGGACTGTACTATTCCCTTTGA  
ATGGTTCATCCGCTTCTGAGGATGAATCCAGTCATTCCATAAGCGGAATTCCAG  
TTCTAAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATCAGCCTGAGGTTCTGTGG  
TCGGATGGTACGGAGGAGCACCGGATCAAACTGGAACAGCACAGGCTCTGGCCTGGTT  
ATATAATGAAAGCCCAGTCCGGGCACAGTAGTCACCAATGATCGTTGGGAGCTGGTAGCA  
TCTGTAAGCATGGTGGCTCTACCTGCAGTGATCGTTATAACCCAGGACATCTTGCCA  
CATAAATGGAAAACGTGACATGACAATAGACAAACTGTCTGGGCTATAGGAGGAAAGCTGG  
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTCATGTG  
GAGGAAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTTCTGTAGTTTGAG  
GAGCGACTGAGGCAAGTGGGTCCTGGCTAAAGTCATGGAGAAGCTATTATGAAACCTA  
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG  
AAAAATTAGTCTATGCCATTCTAAATGGCCCACATCAGGACAGCTGTTCTGGCCAT  
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAAC  
GATTCTTGAGAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCAGATGC  
CGTGTAAATGGGGCTGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG  
ATGCTGCAAGTTATGCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA  
AAGCAATGTAACGGATAAGAAAATTATGGCAGTTCAAGGCTTCCCTTTCCCAC  
AATTCTTAAATTACCCATGTAACCATTAACTCTCCAGTGCACTTGCCATTAAAGTC  
TCTTCACATTGATTGTTCCATGTGTGACTCAGAGGTGAGAATTTCACATTAGTAG  
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTGTGAAGCCATATCCCCCATG  
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGAAATGCATTGCTAGTCAT  
TTTTTTGTGCCAACATCATAGAGTGTATTACAAACCTAGATGGCATAGCCTACTACA  
CACCTAATGTGTATGGTATAGACTGTCCTAGGCTACAGACATATAAGCATGTTACTG  
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG  
GTACAGTAAAATACTGTAAAATAATGGTGCACCTGTATAGGGCACTTACCCAGGAATGGAG  
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA  
TTGAAACACTGCCAGACGTTATAAAACTGTATGCTTAGGCTACACTACATTATAAAAAAAA  
GTTTTCTTCTTCAATTATAAAATTAAACATAAGTGTACTGTAACTTACAAACGTTTAATT  
TTTAAACCTTTGGCTTTGTAATAACACTTAGCTAAACATAAAACTCATTGTGCAA  
ATGTAA

## **FIGURE 72**

MRPQELPRLAFPLLLLLLPPPPCAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHG  
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS  
GAKYIVLTSKHEGFTLWGSEYSWNNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLFEW  
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY  
NESPVVRGTVVTNDRGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI  
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT  
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI  
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

**Signal sequence:**

amino acids 1-28

□ N-glycosylation site.  
□ amino acids 171-175, 239-243, 377-381

□ Casein kinase II phosphorylation site.  
□ amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,  
375-375

□ Tyrosine kinase phosphorylation site.  
□ amino acids 361-369, 389-397

N-myristoylation site.  
amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.  
amino acids 410-432

Alpha-L-fucosidase putative active site.  
amino acids 283-295

## **FIGURE 73**

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGT  
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGGCCATC  
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGCCAGGTGCTTCAGCCTGGTGTG  
CTTCTCACTCCATCTGGACCAACGAGGCTCTGGTCCAAGGCTCTTGCGTGAGAAGAGCT  
TTCCATCCAGGTGTCACTGCAGAATTATGGGGATCACCCTGTGAGCAAAAGGCGAACAGC  
AGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCCGGCAAG  
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAACACTGCAGCTATGGCTGGGTGGAGA  
TGGATTCGTGGTCATCTCTAGGATTAGCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTG  
TCCTGATTGGAAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACACTCATCTGAT  
ACTTGGACTAACTCGTCATTCCAGAAATTATCACCAACCAAAGATCCCATAATTCAACACTCA  
AACTGCAACACAAACAGAATTATTGTCACTGACAGTACCTACTCGGTGGCATCCCCCTT  
ACTCTACAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTCCACTTCTATTCCACGG  
AGAAAAAAATTGATTGTGTCAAGAAGTTTATGGAAACTAGCACCATGTCTACAGAAAC  
TGAACCATTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCC  
CCACGGCTCTGCTAGTGCTTGCCTCCTCTTGGTGTGAGCTGGCTTGGATTTC  
TATGTCAAAAGGTATGTGAAGGCCTCCCTTACAAACAAGAATCAGCAGAAGGAAATGAT  
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTAATGAGGAATCAAAGA  
AAACTGATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACCTACCGTGCATGCCTGGAA  
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC  
TTACCCCTGCCCTAGCTGGGAAATCAAAAGGCCAAAGAACCAAAGAACAGAAAGTCCACCCCTT  
GGTTCTTAACGGAAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAACAGAAC  
CCTTCTCCTTATTGTAACCCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTCCACGGCC  
TTTCTAGCCTGGCTATGCTTAATAATATCCACTGGAGAAAGGAGTTTGCAAAGTGCAA  
GGACCTAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTGAGGCTAGG  
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTACTGATTCCGAGCTCAGAC  
CCTTCTCAGCTCTGAAAGAGAAACACGTATCCACCTGACATGTCCTCTGAGCCGGTA  
AGAGCAAAAGAACGGAGAAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG  
ACCTAATCTCTGTAAGCTAAAATAAAGAAATAGAACAAAGGCTGAGGATAACGACAGTACACT  
GTCAGCAGGGACTGTAACACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGGA  
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTCT  
AGGAAATATACTTTACAAGTAACAAAATAAAACTCTTATAAATTCTATTCTATCTGA  
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA  
ACAAACATTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT  
TGAATATTATTCCCTCAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTCT  
GTTTGATATTCTAGCTTACTTCCAAACTAATTCTATTGCTGAGACTAATCTT  
ATTCACTTCTCTAATATGGCAACCATTATAACCTTAATTATTAAACATACCTAACAG  
TACATTGTTACCTCTATATACCAAGCACATTAAAAGTGCCTAACAAATGTATCACTA  
GCCCTCCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGTGACAAAAATTAA  
AGCATTAGAAAATT

## **FIGURE 74**

MARCFSLVLLLTSIWTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR  
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNSPKCGKNGVGVLIWKVPVSRQF  
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP  
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAASFKNAAAGFGGVPTALLVLALLFF  
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP  
SKTTVRCLEAEV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site.**

amino acids 79-88

**N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## **FIGURE 75**

AGATGGCGGTCTTGGCACCTTAATTGCTCTCGTATTGGTGCACGACTTACGATGG  
CTCGCCCAACCTTACTACCTTCTGTCGGCCCTGCTCTGCTGCCTCCTACTCGTGAGGAA  
ACTGCCGCCGCTCTGCCACGGCTGCCACCCAACGCGAAGACGGTAACCGTGTGACTTTG  
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCATTGTGATGATGAAGAACCGCAGA  
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCAAACACAAT  
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC  
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA  
ACCATTGATGAGGAACTAGAACGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTGCCAA  
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC  
GTACAGGGCTAAATTTGGGAAGGTGGATGTGGACGCTACTGATGTTAGTACGGTAC  
AAAGTGAGCACATCACCCCTACCAAGCAACTCCCTACCCGTACCTGTTCCAAGGTGGCAA  
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTCTCG  
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGCGGCCAAGAAACTATCA  
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTCAACCCCCACCAAGTGTCAATT  
TGGGGAAAACAAGAAGGATAAAAGATCCTCACTTGGCAGTGCTCCTCTCCGTCAATT  
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTCCCTTGG  
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTAAAGAGGCATCTAGGGATTGTCAG  
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCCAAGTGTGTTCACTGGAGCAAGAAAGAGATC  
TCATAGGACGGAGGGGGAAATGGTTCCCTCCAAGCTGGTCAGTGTGTTACTGCTTATC  
AGCTATTAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCCCTTTAG  
TTGACCTGCACAGCTGGTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGTATAGAA  
CGCTAAGAATTTCCCCCAAGGACTCTGCTTCTTAAGCCCTCTGGCTTGTGTTATGGTC  
TTCATTAAAAGTATAAGCCTAACCTTGTGCTAGTCCTAACGGAGAAACCTTAACCACAAAG  
TTTTTATCATTGAAGACAATATTGAACAACCCCCCTATTGTGGGATTGAGAAGGGGTGAA  
TAGAGGCTTGAGACTTCCCTTGTGGTAGGACTTGGAGGAGAAATCCCTGGACTTCAC  
TAACCCCTTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT  
TCCTTTG

## **FIGURE 76**

MAVLAPLIALVYSPRLSRWLAQPYYLLSALLSAFLVRKLPPCHGLPTQREDGNPCDFDWREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFLMTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE ENVIREFNLNELYQRAKKLSAGDNIPEEOPVASTPTTVSDGENKKDK

### Signal sequence:

amino acids 1-48

### Transmembrane domain:

amino acids 111-125

### N-glycosylation site.

amino acids 165-169, 185-189

## cAMP- and cGMP-dependent protein kinase phosphorylation site

amino acids 154-158, 265-269

### Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

### N-myristoylation site.

amino acids 188-194, 225-231

### Myb DNA-binding domain repeat signature 1.

amino acids 244-253

## **FIGURE 77**

GGACAGCTCGCGCCCCGAGAGCTAGCCGTCGAGGAGCTGCCCTGGGACGTTGCCCTG  
GGGCCAGCCTGGCCGGTCACCCCTGGCATGAGGAGATGGCCTGTTGCTCCTGGTCCA  
TTGCTCCTGCTGCCCGCTCCTACGGACTGCCCTCTACAACGGCTTACTACTCCAACAG  
CGCCAACGACCAGAACCTAGGCAACGGTACGGCAAAGACCTCTTAATGGAGTGAAGCTGG  
TGGTGGAGACACCCGAGGAGACCCCTGTTCACCTACCAAGGGCCAGTGTGATCCTGCCCTGC  
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGGCGGTGTGCGTGTCAAATGGTGGAAAGCT  
GTCGGAGAACGGGCCAGAGAGAAGGACGTGCTGGTGGCCATCGGCTGAGGCACCGCTCCT  
TTGGGACTACCAAGGCCGGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG  
ATCCAGGATCTGCGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTATTGACGGCTGGA  
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGGGGGTGTGGTCTTCCTTACCAAGTCCCCA  
ACGGCGCTACCAGTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCCGTG  
GTGGCCTCTTGAGCAGCTCTCCGGGCCTGGGAGGGAGGGCTGGACTGGTGCAACGCCGG  
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGGCAGCCCTGCCGTGGC  
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACGCCGCTGCACCGCTATGAT  
GTATTCTGCTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCTGAGAAGCT  
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGAC  
AGCTTTGCCGCCTGGAAGTCCATGGCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT  
GGCAGCGTCCGCTACCCGTGGTCACCCGCATCCTAACTGTGGGCCCCAGAGCCTGGGT  
CCGAAGCTTGGCTCCCCGACCCGCAGAGCCGCTGTACGGTGTACTGCTACCGCCAGC  
ACTAGGACCTGGGCCCTCCCTGCCGCATCCCTCACTGGCTGTATTGAGTGGTT  
CGTTTCCCTGTGGTTGGAGCCATTAACTGTTTATACTTCTCAATTAAATTCT  
TTAACATTTTTACTATTTTGAAAGCAAACAGAACCCATGCCCTCCCTTGCTCCTG  
GATGCCCACTCCAGGAATCATGCTGCTCCCTGGGCCATTGCGGTTTGCTGGCTTCTG  
GAGGGTCCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGGCCAGAGTGGC  
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGCATGGTGGCACAGTCTCCCTGCC  
CAGCCTGGGGAAAGAAGAGGGCCTGGGGGCCCTCCGGAGCTGGCTTGGCCTCTGCC  
CACCTCTACTCTGTGAAGCCGCTGACCCAGTCTGCCACTGAGGGCTAGGGCTGGAA  
GCCAGTTCTAGGCTCCAGGCAGAACATGAGGAAGGAAGAAACTCCCTCCCCGTTCC  
TCCCTCTCGGTTCAAAGAATCTGTTGTCATTGTTCTCCTGTTCCCTGTGTGG  
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGCTATGACTGCCCTCGCCAA  
AA  
AA

## **FIGURE 78**

MGLLLVPLLLPGSYGLPYNGFYYNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ  
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFVQSPNGRYQFNFHEGQQ  
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGP  
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

**Signal sequence:**

amino acids 1-17

**Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

**Tyrosine kinase phosphorylation site.**

amino acids 137-145

**N-myristoylation site.**

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

## **FIGURE 79**

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGGATGATGTGGCGACCATCAGTTCTGCTGC  
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC  
CAGGGGAGGGTGCACCAGGCGCCCCCTGAGCGACGCTCCCCATGATGACGCCACGGAA  
CTTCCAGTACGACCATGAGGCTTCCTGGACGGGAAGTGGCAAGGAATTGACCAACTCA  
CCCCAGAGGAAAGCCAGGCCGTCTGGGCGGATCGTGGACCGCATGGACCGCGGGGGAC  
GGCGACGGCTGGGTGTCGCTGGCGAGCTCGCGCTGGATCGCGCACACGCAGCAGCGCA  
CATACGGGACTCGGTGAGCGCGCCTGGACACGTACGACACGGACCGCGACGGCGTGTGG  
GTTGGGAGGAGCTCGCAACGCCACCTATGCCACTACCGCCGGTGAAGAATTGAC  
GTGGAGGATGCAGAGACCTACAAAAGATGCTGGCTCGGACGAGCGGCGTTCCGGGTGGC  
CGACCAGGATGGGACTCGATGCCACTCGAGAGGAGCTGACAGCCTCCTGCACCCCGAGG  
AGTCCCTCACATGCGGACATCGTATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAAA  
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGAGGA  
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTCCGGACTTCCGGATCTGAACAAGG  
ATGGGCACCTGGATGGAGTGAGGTGGCCACTGGTGCTGCCCTGCCAGGACCAGCCC  
CTGGTGGAAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGGCTGAGCAA  
AGCGGAAATCCTGGTAATTGAAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG  
ACCTGACCCGGCACACGATGAGCTTGAGCCACCGCACCTGCCACAGCCTCAGAGGCCG  
CACAATGACCGGAGGAGGGCCGCTGGTCTGCCCTCCCTGTCCAGGCCCGCAGGAG  
GCAGATGCAGTCCCAGGCATCCTGCCCTGGCTCTCAGGGACCCCTGGGTCGGCTTC  
TGTCCCTGTCACACCCCAACCCAGGGAGGGCTGTCATAGTCCCAGAGGATAAGCAATAC  
CTATTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCCTGCCAGGAAAGCTCAGCTCTAA  
GAACCGCCCCAACCCCTCCAGCTCAAATCTGAGCCTCCACCATAGACTGAAACTCCCT  
GGCCCCAGCCCTCTGCCCTGGCCTGGACACCTCCTCTGCCAGGAGGAATAA  
AAGCCAGCGCCGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAA

## **FIGURE 80**

MMWRPSVLLLLLRLHGAQGKPSPDAGPHQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR  
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT  
YDTDGRVGWEELRNATYGHYAPGEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE  
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ  
FRDFRDLNKGHLDGSEVGHVLPPAQDQPLVEANHLLHESDTDKDGRSLKAEILGNWNMFV  
GSQATNYGEDLTRHHDEL

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 140-144

**Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

**N-myristoylation site.**

amino acids 263-269, 311-317

**Endoplasmic reticulum targeting sequence.**

amino acids 325-330

## **FIGURE 81**

GGGGCCTTGCCTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGC GGAGCCCCGG  
GCGGCAGGGCGCGGGTGCAGGGGATCCCTGACGCCTCTGTCCCTGTTCTTGTGCTCCCAG  
CCTGTCTGTCGTTGGCGCCCCGCTCCCCGCGGTGCGGGGTTGCACACCGATCCTG  
GGCTTCGCTCGATTGGCGCCGAGGGCGCTCCCAGACCTAGAGGGCGCTGGCCTGGAGCAG  
CGGGTCGTCGTTGTCCCTCTCCCTCTGCGCCGCCGGGATCCGAAGGGTGC GGGGGCTCT  
GAGGAGGTGACCGCGGGGCCTCCCAGCACCCTGGCCTGCCCCTCCTCCCAG  
GTGTGAGCAGCCTATCAGTCACCATGTCCGCAGCCTGGATCCGGCTCTGGCCTCGGTGTG  
TGTCTGCTGCTGCCGGGCCCGGGCAGCGAGGGAGCCGCTCCCATTGCTATCACATG  
TTTACAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCAGGGGGCTGCC  
CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTCTGTATCGAGCATATGTGG  
GCTGCTGTCACAGGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC  
TGGTCGAGAAAACATTCCCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTCTAGAT  
GGTCTGCTCTTCACAGTAACAAAGGCAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAACGG  
CAATAAAGATTGTAAAGCAGACATTGCATTTGATTGATGGAAGCTTAATATTGGCAGC  
GCCGATTTAATTACAGAAGAATTGGTGTGAAAGTGGCTCTAATGTTGGAAATTGGAACA  
GAAGGACCACATGTGGCCTTGTCAAGCCAGTGAACATCCAAAATAGAATTACTTGAA  
AAACTTACATCAGCAAAGATGTTGTTGCCATAAAGGAAGTAGGTTCAGAGGGGTA  
ATTCCAATACAGGAAAAGCCTGAAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA  
GTAAGAAAAGGGATCCCCAAAGTGGTGGTATTATTGATGTTGGCCTCTGATGACAT  
CGAGGAAGCAGGCATTGTGGCAGAGAGTTGGTGTCAATGTATTAGTTCTGTGGCCA  
AGCCTATCCCTGAAGAACTGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGCTGT  
CGGAATAATGGCTTCTCTTACCATGCCAACTGGTTGGCACCAAAATACGTAAA  
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAAGCACCTGTTATAACT  
CAGTGAACATTGCCCTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTCCGCC  
ATGCTTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTCGGACATTGGTGCCAAGAT  
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCACTGACTATAGCACCA  
AAGAGAATGTCCTAGCTGTCACTAGAAACATCCGCTATATGAGTGGTGGAAACAGCTACTGG  
GATGCCATTCTCACTGTTAGAAATGTGTTGGCCCTATAAGGGAGAGCCCCAACAGAA  
CTTCCTAGTAATTGTCACAGATGGGCAGTCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG  
CACATGATGCAGGAATCACTATCTCTGTGGTGTGGCTGGCACCTCTGGATGACCTG  
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTCTTACAAGAGAGTTCACAGGATT  
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGAGAGATTCTTACAATCCCAGCAAT  
ATGGTAACATTGACAACGTAAAGAAAAAGTACAAGGGGATCCAGTGTGTAATTGTATT  
CTCATAACTGAAATGCTTACTGATGAGATCAGATAACAAACTATTAAGTATGTCAAC  
AGCCATTTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCTCTGGTTACAATTACAGTGT  
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTTCTAGAAACTCAGGAAAGAGGA  
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAA  
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAAA

## FIGURE 82

MSAAWI PALGLGVCLLLLPGPAGSEGA APIA ITCFTRGLDIRKEKADVLCPGGC PLEEF SVY  
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT  
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDKCKADIAFLIDGSFNIGQRRFNLQKN  
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAIKEVGFRGGNSNTGKAL  
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSSDIEEAGIVAREFGVNVFIVSVAKPIPEELG  
MVQDVTFVDKAVCRNNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI  
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTESFTDYSTKENVLAVI  
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI  
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

**Signal sequence:**

amino acids 1-24

**N-glycosylation site.**

amino acids 100-104, 221-225

**Casein kinase II phosphorylation site.**

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,  
425-429, 478-482, 528-532

**N-myristoylation site.**

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

**Amidation site.**

amino acids 145-149

## **FIGURE 83**

CGCCCGCGCTCCCGCACCCGGCCCGCCACCAGCGCCGCTCCCGCATCTGCACCCGAGCCC  
GGCGGCCTCCCGCGGGAGCAGCAGATCCAGTCCGGCCCGAGCGCAACTCGGTCCAGTCG  
GGGCGGCGGCTGCGGGCGAGAGCGGAGATGCAGCGGCTTGGGCCACCCCTGCTGTGCCTGC  
TGCTGGCGGCGGCGGTCCCCACGGCCCCCGCGCCCGCTCCGACGGCGACCTCGGCTCCAGTC  
AAGCCCGGCCCGGCTCTCAGCTACCCGAGGAGGAGGCCACCCCTCAATGAGATGTTCCGCGA  
GGTGAGGAAGTGTGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG  
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACACTACCTCCCAGCTAT  
ACAATGAGACCAACACAGACACGAAGGTTGAAATAATACCATCCATGTGCACCGAGAAAT  
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG  
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTCATCATCGACGAGGACTGTGGGCCAGC  
ATGTACTGCCAGTTGCCAGTTCCAGTACACCTGCCAGCCATGCCGGGGCAGAGGATGCT  
CTGCACCCGGGACAGTGGAGTCAGCTGTGGAGACCAGCTGTGTCTGGGTCACTGCACCAAAA  
TGGCCACCAGGGGAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG  
TGCTGTGCCTTCCAGAGAGGGCTGCTGTTCCCTGTGTCACACCCCTGCCGTGGAGGGCGA  
GCTTGCCATGACCCGCCAGCCGGCTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG  
GAGCCTTGGACCGATGCCCTGTGCCAGTGGCCTCCTGCCAGCCCCACAGCCACAGCCTG  
GTGTATGTGTGCAAGCCGACCTCGTGGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC  
CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGG  
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCGCTGCCGCCGCT  
GCAGTGTGGAGGGAGAGATTAGATCTGGACCGAGGCTGTGGTAGATGTGCAATAGAA  
ATAGCTAATTATTCCCCCAGGTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT  
TCTTCTTCCCAGTAAGTTCCCCTCTGGCTTGACAGCATGAGGTGTTGCTTGTGCTTGTGCT  
TCCCCCAGGCTGTCTCCAGGCTTCACAGTCTGGCTGTGGAGAGTCAGGCAGGGTTAAC  
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTCTACCAAGTTGGCAG  
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGAAACAATGTGG  
AGTCTCCCTGTGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGTGCAAACATCAA  
CCTGGCAAAATGCAACAAATGAATTTCACAGCAGTTCTTCCATGGCATAGGTAAGCTG  
TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTCACTACATGTGTTATTGATCC  
AGCAGTGTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATT  
CCTCTCTCAGCACAGCCTGGGAGGGGTATTGTTCTCCTCGCCATCAGGATCTCAGAG  
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTCAT  
CTGGTTGTGACTCTAAGCTCAGTGTCTCTCCACTACCCACACCAGCCTTGGTGCCACCAA  
AAAGTGTCCCCAAAAGGAAGGAGAATGGGATTCTTGAGGCATGCACATCTGGAATTAAG  
GTCAAACATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC  
AGTGTGGGGCAGCGTCCCTCTAATGAAGACAATGATATTGACACTGTCCCTCTTGGCAGT  
TGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCATAACAGGTTAACCTGCAGAAACA  
GTACTTAGTAATTGTAGGGCGAGGATTATAATGAAATTGCAAATCACTTAGCAGCAAC  
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGAAACATGGTT  
GTAATATGCGACTGCCAACACTGAACACTACGCCACTCCACAAATGATGTTTCAGGTGTCA  
TGGACTGTTGCCACCATGTATTGACACTGTCTTAAAGTTAAAGTTGACATGATTGTA  
TAAGCATGCTTCTTGAGTTAAATTATGATAAACATAAGTTGCATTAGAAATCAAGC  
ATAAATCACTCAACTGCAAAAAAAAAAAAAAA

## **FIGURE 84**

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ  
HKLRSAVEEMEAEEAAKASSEVNLNLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTG  
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRSECCG  
DQLCVWGHCTKMATRGSGNTICDNQRDCQPGLCCAFQRGLFPVCTPLPVEGELCHDPASRL  
LDLITWELEPDGALDRPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGIELLPREVPDEYEV  
GSFMEEVROELEDLERSLTEEMALGEPAAAAALLGGEI

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristoylation site.**

amino acids 202-208, 217-223

**Amidation site.**

amino acids 140-144

## FIGURE 85

AAGGAGGGCTGGGAGGAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTGGCTCAGAAGGACTCTG  
AAGATAACAATAATTCAAGCCCATCCACTCTCCTTCCCTCCAAACACACATGTGCATGTACACACACATACA  
CACACATACACCTTCCTCTCCTTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCAAGAAAAGGACAC  
TAAAGCCTTAAGGCAGGGCTGGCATTACCTCTGCAGCTCTTGGCTTGTGAGTCAGAAAACATGGAGGG  
CCAGGCACGGTCACTCACACCTGTAATCCCAGCATTGGAGACCGAGGTGAGCAGATCACTTGAGGTCAAGGAG  
TTCGAGACGGCTGGCAGGAAACATGGAGAAACCCCCATCTACTAAACAAAATTAGCCAGGAGTGGTGGC  
AGGTGCCTGTAATCCCAGCTACTCAGGTGGCTGAGCCAGGAGAATCGCTGAAATCCAGGAGGGAGGATGCCAGT  
CAGCTGAGTCACCGCTGCACTCCAGCCTGGGAGCAGAATGAGACTCTGTCTCAAACAAAACACGGGAGGA  
GGGGTAGATACTGCTTCTGCAACCTCTTAACCTCTGCACCTCTTCCAGGGCTGCCCCCTGATGGGGCCTG  
GCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGAAGAGAACGGCATATTGAGGAGGGCAAGAAGTGACGCCG  
GTGAGAATGACTGCCCTGGGAGGGTGGTCCCTGGGAGGGTGTGACCCCTACCCCTGCAAAACAC  
AAGAGCAGGACTCCAGACTCTCCTGTGAATGGTCCCCCTGCCCCAGCTGAGCTCAGATGAGGCTTCTCGTGGCCCC  
ACTCTGCTAGCTGGGGCTGGCTGGCACTGCCACTGTGCCAGCTGGTACCCCTGGCATGTTCCCTGCCCCCTCA  
GTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCGCTGCTCTACCGCGAGGCTACCAACTGTGGACTGCAATGA  
CCTATTCTGACGGCAGTCCCCCGGCACTCCCCGAGGCACACAGACCCCTGCTGAGGCAACAGCAATTGT  
CCGTGTGGACCAGAGTGAAGCTGGCTACCTGGCAATCTCACAGAGCTGGACTGTCCCAGAACAGCTTTGGA  
TGCCCGAGACTGTGATTCCATGCCCTGCCAGCTGCTGAGCCTGACCTAGAGGAGAACAGCTGACCCGGCT  
GGAGGACCACAGCTTGAGGGCTGGCAGCCATAGGAACACTATCTCAACCACAACCAGCTCACCGCATCGC  
CCCCAGGGCCTTCTGGCCTCAGCAACTTGCTGCCGTGACCTCAACTCCAACCTCTGAGGGCATTGACAG  
CCGCTGGTTGAAATGCTGCCAACCTGGAGATACTCATGATTGGGGCAACAGGTAGATGCCATCTGGACAT  
GAACCTCCGGCCCTGGCCAACCTGCGTAGGCTGGTGTAGCAGGCATGAACCTGCCGGAGATCTCGACTATGC  
CCTGGAGGGCTGCAAAGCCTGGAGAGCCTCTCCTTCTATGACAACCAAGCTGCCCGGGTGCCCAGGCGGGCACT  
GGAACAGGTGCCGGCTCAAGTCTCTAGACCTCAACAAGAACCCGCTCCAGCGGGTAGGGCGGGGACTTGC  
CAACATGCTGACCTTAAGGAGCTGGACTGAACAACATGGAGGAGCTGGCTCCATGACAAGTTGCCCCTGGT  
GAACCTCCCCGAGCTGACAAGCTGGACATACCAATAACCCACGGCTGTCCTTCTATCCACCCCCCGCCTTCA  
CCACCTGCCAGATGGAGAACCTCATGCTCAACAAACAGCTCTCAGTGCCCTGCACCCAGCAGACGGTGGAGTC  
CCTGCCCAACCTGCAAGGGTAGGTCTCACGCCAACCCATCCGCTGTGACTGTGTCATCCGCTGGGCCATG  
CACGGGACCCGTGTCGCCCTCATGAGCCGAATCCACCCCTGTGAGGCTCCAGCAGCGCCTCCC  
GGTCCGTGAGGTGCCCTTCCGGAGATGACGGACCAGTGTGCCCCCTCATCTCCCAGAACAGCTTCCCCCAAG  
CCTCAGGTAGCCAGTGGAGAGAGCATGGTGTGCAATTGCCGGCACTGGCCGAACCCGAACCCGAGATCTACTG  
GGTCACTCCAGCTGGCTCGACTGACACCTGCCATGCAGGCAGGAGGTACGGGTGTACCCCGAGGGACCC  
GGAGCTGCCGGAGGGTGACAGCAGAACAGGGCAGGGCTATACACCTGTGTGGCCAGAACCTGGTGGGGCTGACAC  
TAAGACGGTTAGTGTGGTGTGGCCGTGCTCCTCCAGCCAGGAGGGCAGAACGGAGGACAGGGCTGGAGCTCCG  
GGTGCAGGAGACCCACCCCTATCACATCTGCTATCTGGGTCAACCCACCCAACACAGTGTCCACCAACCTCAC  
CTGGTCCAGTGCCCTCCCTCCGGGCCAGGGGCCACAGCTGGCCCTGCCTGGGGAACCCACAGCTA  
CAACATTACCCGCTCCTCAGGCCACGGAGTACTGGCCCTGCCATGAGCTGGCCCTTGTGATGCCACACCC  
GTTGGCTTGTGTATGGGCAGGACCAAAAGAGGCCACTCTTGCACAGAGCCTAGGGGATGTCCTGGCTCAT  
TGCCATCTGGCTCGCTGTCTTCTCCGGCAGCTGGCTAGGGCCACCTGGCACAGGCCAACCCAGGAA  
GGGTGTGGGTGGGAGGCGGCCCTCCCTCCAGCCTGGCTTCTGGGCTGGAGTGCCCTCTGTCCGGGTTGT  
GTCTGCTCCCTCGTCTGGCCCTGGAAATCCAGGGAGGAAGCTGCCAGATCTCAGAACGGGAGACACTGTTGCC  
ACCATTGTCTAAATTCTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTACCAA  
AGAGAACAGCTGGGCCAGATGCCCTGCCAGGAAGGGACATGGACCCACGTGCTGAGGGCTGGCAGCTGGC  
CAAGACAGATGGGCTTGTGGCCCTGGGGGTCTCTGCAGCCTGAAAAAGTGTGCCCTTACCTCTAGGGTCA  
CCTCTGCTGCCATTCTGAGGAACATCTCAAGGAACAGGAGGGACTTGGCTAGAGCCTCTGCCTCCCCATCTT  
CTCTGCCCCAGGGCTCTGGCTTGTGCTCTGGCTTGTGCTCTGGCAAGGGCTGAAGGGAGGCCACTCCATCTCAC  
TCTTCTCTGTACAGTCTCAGTTGCTTGTGCTCTGGCTTGTGCTCTGGCAAGGGCAGATCTGAAGGGACATTGGGAGGGATGCCAGGAA  
CTCGGGGGCTGCCCTCAATGTGGGAGTGACCCAGCCAGATCTGAAGGGACATTGGCAATTGGTACCTTGTGAGGAA  
CGCCTCATCTCAGCAGCTGGCTGGCATTCCGAAGCTGACTTTCTATAGGCAATTGGTACCTTGTGAGGAA  
ATGTGTACACCTCCCCAACCCGATTCACTCTTCTCTGGTAAAAAATAAAATAACAATAAAA  
AAAA

## **FIGURE 86**

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA  
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQQLSLHL  
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE  
MLPNLEILMIGGNKVDAILDMNFRPLANLRSILVLAGMNLREISDYALEGLQSLSLFYDNO  
LARVPRRALEQVPGLKFLDLNKNPLQRVPGDFANMLHLKELGLNNMEELVSIKFALVNLP  
ELTKLDITNNPRLSFIHPRAFHHLQPQMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIR  
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ  
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHGRRYRVYPEGTLELRRVTAAEAGLYT  
CVAQNLVGADEKTVSVVGRALLQPGGRDEGQGLELRVQETHPYHILLSWTPNNTVSTNLTW  
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS  
CHRALGDRPGLIAILALAVLLAAGLAAHLGTGQPRKGVGRRPLPPAWAFWGWSAPSVRVV  
SAPLVLPWNPGRKLPSSGETLLPPLSQNS

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 629-648

**N-glycosylation site.**

amino acids 94-98, 381-385, 555-559, 583-587

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 485-489

**Casein kinase II phosphorylation site.**

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,  
243-247, 313-317, 488-492, 700-704

**Tyrosine kinase phosphorylation site.**

amino acids 532-540

**N-myristoylation site.**

amino acids 15-21, 493-499, 566-572

**Amidation site.**

amino acids 470-474, 660-664, 692-696

## **FIGURE 87**

GCAAGCCAAGGGCTGTTGAGAAGGTGAAGAAGTCCGGACCCATGTGGAGGAGGGGACATTGTGTACCGCCT  
CTACATGCGGAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGCTACTACGTGCACAA  
CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCACCC  
CCTGCCACACTCTTCAGATCCTGGCGTCTTCTACATCAGCTAGTCATCTTACGGCCTCATCTGCATGTA  
CACACTGTGGTGGATGCTACGGCCTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTGAGGAGAGCAGCTACAG  
CGACATCCCCGACGTCAAGAACGACTTCGCCTTATGCTGCACCTCATTGACCAATACGACCCGCTACTCCAA  
GCGCTTCGCCGCTTCTGCGGAGGTGAGTGAGAACAGCTGCGCAGCTGAACCTCAACAACGAGTGGAGCCT  
GGACAAGCTCCGGCAGCGCCTACCAAGAACCGCAGGACAAGCTGGAGCTGCACCTGTCAGTGGCAT  
CCCTGACACTGTGTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCGCC  
CAGCATTGCCAGCTCACGGGCTCAAGGAGCTGTTGACCATCAAGGAGCTGACCTCATTGACCAATACGCGCCTGCC  
GGCCTTCTGCGCAGAACCTGCGGGCGTGCACATCAAGTTCACCGACATCAAGGAGATCCCGCTGTGGATCTA  
TAGCTGAAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACAAACCGCTACATCGTCATCGA  
CGGGCTGCCGGAGCTCAAACGCCCTCAAGGCTGCTGCCCTCAAGAGAACCTAACAGGAGCTGACAGGTGGTAC  
AGATGTGGCGTGCACCTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCATTTCAAGCCTAA  
GAAGATGGCGAACCTGACTGAGCTGGAGCTGACCTCAAGGACAACACCTCAAGACCATCGAGGAGATCATCAGCTCCAGCACCT  
GCACCGCCTCACCTGCCTTAAGCTGGTACAACCACATCGCCTACATCCCCATCCAGATCGGCAACCTCACCAA  
CCTGGAGGCCCTTACCTGAAACGCAACAAGATCGAGAACAGATCCCCACCCAGCTTCTACTGCCGCAAGCTGCG  
CTACCTGGACCTCAGCCACAACACCTGACCTTCTCCCTGCCGACATCGGCTCTGCAAGAACCTCCAGAACCT  
AGCATCACGGCAACCGGATCGAGACGCTCCCTCCGGAGCTTCCAGTGCAGGAGCTGCGGGCCCTGCACCT  
GGGCAACAAACGTGCTGCAGTCAGTCACTGCCCTCCAGGGTGGCGAGCTGACCAACCTGACGCAAGATCGAGCTGCC  
CAACCGGCTGGAGTGCCTGCTGTGGAGCTGGCGAGTGCCTACTGCTCAAGCGCAGCGCTTGGTGGAGGA  
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCCCTGAGCGAG  
GCCGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCCTCAGGCCGGAGGGGAGGCCCTAGCTTCTCCAG  
AACTCCCGGACAGCCAGGACAGCCTCGCGCTGGCAGGGCCTGGGAGCTGGGAGCTGAGTCAGGCCAGAGCGAGA  
GGACAGTATCTGTGGGCTGGCCCTTCTCCCTGAGACTCACGTCCCCAGGGCAAGTGTCTGTGGAGGAG  
AGCAAGTCTCAAGAGCGCAGTATTTGATAATCAGGGTCTCCTCCCTGGAGGCCAGCTCTGCCAGGGGCTGAG  
CTGCCACCAGAGGTCTGGACCCCTCACTTAGTTCTGGTATTATTTCTCCATCTCCACCTCCTTCACTCC  
AGATAACTTATACATCCCAAGAAAGTTGAGCCAGATGGAAGGTGTTCAAGGAAAGGTGGCTGCTTCTTCCCC  
TTGCTCTTATTAGCGATGCCGCCGGCATTTAACACCCACCTGGACTTCAGCAGACTGTCAGGGCGAACCAG  
CCATGGGACGGTCACCCAGCAGTGCCTGGCTCTGCCGCTGGGAGAGCAGGCCCTCAGCTGGA  
AAGGCCAGGCCCTGGAGCTGCCCTTCAGTTTGTCAGGTTAGTTTTGTTTTTTTTTTTTAATCAA  
AAACAATTTTTAAAAAAAGCTTGAAATGGATGGTTGGGTATTAAAAAGAAAAAAACTTAAAAAA  
AAAAGACACTAACGCCAGTGAAGTGGAGTCTCAGGGCAGGGTGGCAGTTCCCTTGAGCAAAGCAGCCAGACGT  
TGAACGTGTTCTTCCCTGGCGCAGGGTGCAGGGTGTCTTCCGGATCTGGTGTACCTTGGTCCAGGAGTT  
CTATTGTTCTGGGAGGGAGGTTTTGTTGTTGGTTTTGGTGTCTTGTCTTCTCC  
ATGTGTCTGGCAGGCACTCATTCCTGTTGCTGCGGCCAGAGGGAAATGTTCTGGAGCTGCCAAGGAGGGAGGAG  
ACTCGGGTGGCTAATCCCGGATGAACGGTGTCCATTGCCACCTCCCTCGTGCCTGCCCTGCCCTCCA  
CGCACAGTGTTAAGGAGCCAAGAGGAGCCACTCGCCAGACTTGTGTTCCCCACCTCCTGCCGATGGGTGTT  
CCAGTGCCACCGCTGGCCTCCGCTGTTCCATCAGCCCTGTCGCCACCTGGTCTTCTAGAACAGAGCAGACACTTA  
GAGGCTGGTGGGAATGGGAGGTGCCCTGGAGGGCAGGCCTGGTTCCAAGCCGGTCCCTGGCCTGCC  
CTGGAGTGCACACAGCCAGTCGGCACCTGGTGGCTGGAGGCCAACCTGTTAGATCACTGGGCCCCACCTT  
AGAAGGGTCCCCGCTTAGATCAATCACGTGGACACTAACGGCACGTTAGAGTCTTTGTCTTAATGATTATGT  
CCATCCGTCTGTCGTCCATTGTTCTGCGTGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG  
CCTCTGACAACCATGAAGAAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAA  
ATCTATAACAGAAAAAA

## **FIGURE 88**

MRQTIKVIKFILIIICYTYYYVHNIKFVDVDCVDIESLTGYRTYRCAHPLATLFKILASFYI  
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSIDPDVKNDFAFMLHLIDQYDPLYSK  
RFAVFLSEVSENKLRLQNLNNNEWTLDKLRQRLTKNAQDKLELHLFMLSGIPDTVFVFLVELEV  
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFDTIKEIPLWI  
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI  
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ  
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPQLFYCRKLRYLDLSHNNLT  
FLPADIGLLQNLQNLAITANRIETLPPPELFQCRKLRALHGNVLQSLPSRVGELTNLTQIE  
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

**Transmembrane domain:**

amino acids 51-75 (type II)

**N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

**Casein kinase II phosphorylation site.**

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497

**N-myristylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

## **FIGURE 89**

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT  
CCCGCGGTGGTTGCTGCTGCCGTGCTGGCCTGAACGCAGGAGCTGTCAATTGACT  
GGCCCACAGAGGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCATACATG  
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT  
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTGGAAACTTGAGGAAATTGGGC  
CCCTTGACAGTGTCAAAACACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATT  
GTGGATAATCCCCTGGGACTGGTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA  
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTCAGTTGCCACAAAG  
AATTCCAGACAGTTCCATTCTACATTTCTCAGAGTCTATGGAGGAAAATGGCAGCTGGC  
ATTGGTCTAGAGCTTATAAGGCCATTCAAGCGAGGGACCATCAAGTGCACACTTGCGGGGGT  
TGCCTGGGTGATTCCCTGGATCTCCCTGTTGATTGGTGCCTCCTGGGACCTTACCTGT  
ACAGCATGTCCTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGGTGCAGAGCAAGTA  
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT  
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACACTAAAGCACTCCCA  
CGTCTACAATGGAGTCGAGTCTAGAATTACACAGAGGCCACCTAGTTGTCTTGTAGCGC  
CACGTGAGACACCTACAACGAGATGCCCTAACGCCAGCTCATGAATGGCCCCATCAGAAAGAA  
GCTAAAATTATTCTGAGGATCAATCCTGGGAGGCCAGGCTACCAACGTCTTGTGAACA  
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC  
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTAGGAGGCCTG  
GGTGGAAACTGAAGTGGCCAGAACTGCCCTAAATTCAAGTCAGCTGAAGTGGAGGCCCTGT  
ACAGTGACCCCTAAATCTTGGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTTC  
TACTGGATTCTGAAAGCTGGTCAATGGTCCCTCTGACCAAGGGACATGGCTCTGAAGAT  
GATGAGACTGGTGAECTCAGCAAGAATTGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT  
TGGGGCACAGAGCTGAGCTGAGGCCCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT  
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGCAGAGGATAAAATCATTGTCTCT  
GGAGGCAATTGGAAATTATTCTGCTTCTAAAAAAACCTAAGATTTTAAAAAAATTGAT  
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

## FIGURE 90

MELALRRSPVPRWLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC  
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY  
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR  
GTIKCNFAGVALGDSWISPVDVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE  
ATELWGKAEMIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS  
QLMNGPIRKKLKIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL  
IVDTMGQEAWRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP  
SDQGDMALKMMRLVTQOE

**Signal sequence:**

amino acids 1-25

**N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

**Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

**N-myristoylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366

## **FIGURE 91**

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC  
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTTATCAGGACCATGC GGCGA  
CGGGTCATCACGTGCGCAGTCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA  
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG  
CACTCACGGCGGCGCACTGCTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG  
GTCCAGTTGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG  
TTACTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAATTCACCTATGACATTG  
CCTTGGTGAAGCTGTCTGCACCTGTACCTACACTAAACACATCCAGCCCATCTGTCTCCAG  
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA  
AGAGGATGAGGCACTGCCATCTCCCCACACCCCTCCAGGAAGTTCAAGTCGCCATCATAACA  
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG  
GTTTGTGCTGGCAACGCCAACGGCGGGAGGATGCCTGCTCGGTGACTCAGGTGGACCCCTT  
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG  
GTCGGCCAATCGGCCCGGTGTCTACACCAATATCAGCCACCACCTTGAGTGGATCCAGAAG  
CTGATGGCCCAAGAGTGGCATGTCCCAGCCAGACCCCTCCTGCCACTACTCTTTCCCTCT  
TCTCTGGCTCTCCACTCCTGGGCCGGTCTGAGCCTACCTGAGCCCATGCAGCCTGGGC  
CACTGCCAAGTCAGGCCCTGGTTCTTCTGTCTTGGTAATAAACACATTCCAGTTGA  
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 92

MGARGALLLALLLARAGLRKPESQEAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW  
DSHVCGVSLLSHRWALTAAHCFETYSDLSPSGWMQFGQLTSMPSFWSLQAYYTRYFVSNI  
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP  
SPHTLQEJVQVIAIINNSMCNHLFLKYSFRKDIIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG  
LWYQIGVVSWGVGCGRPNRPGVYTNISHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL  
LGPV

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 167-171, 200-204, 273-277

**Casein kinase II phosphorylation site.**

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

**N-myristoylation site.**

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,  
259-265, 269-275

**Amidation site.**

amino acids 33-37

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 252-263,

**Serine proteases, trypsin family, histidine active site.**

amino acids 78-84

## **FIGURE 93**

CCACCGCGTCCGGACCGTGGGAAGGGCAGAATGGGACTCCAAGCCTGCCTCTAGGGCT  
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCCAGCCGACCAGCGAGGACGC  
TGCCCCCAGGCTGGGTGCCCCGGACCTGAGGAAGAGCTGAGTCTCACCTT  
GCCCTGAGACAGCAGAATGTGAAAGACTCTCGGAGCTGGTGCAGGCTGTGAGGATCCCAG  
CTCTCCTCAATAACGAAAATACCTGACCCCTAGAGAATGTGGCTGATCTGGTGGAGGCCATCCC  
CACTGACCCCTCCACACGGTCAAAAATGGCTTGGCAGCCGGAGCCCAGAAGTGCATTCT  
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCC  
TGGGCTGAGTTCATCACTATGTGGGAGGACCTACGAAACCATGTTGTAAGGTCCCCAC  
ATCCCTACCAGCTTCCACAGGCCTGGCCCCCATGTGGACTTGTGGGGGACTGCACCGT  
TTTCCCCAACATCATCCCTGAGGCAACGTCTGAGCCGAGGTGACAGGGACTGTAGGCCT  
GCATCTGGGGTAACCCCCTGTGATCCGTAAGCGATACAACCTGACCTACAAGACGTGG  
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCTGGAGCAGTATTTCCATGAC  
TCAGACCTGGCTCAGTTCATGCGCCTTCTGGCAACTTGACATCAGGCATCAGTAGC  
CCGTGTGGTGGACAACAGGGCCGGGGCCGGGATTGAGGCCAGTCTAGATGTGCAGT  
ACCTGATGAGTGCTGGTGCACATCTCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG  
GGACAGGAGCCCTTCCTGCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT  
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCCCTACATCCAGCGGTCA  
█ AACTGAGCTCATGAAGGCTGCCGCTGGGTCTCACCTGCTTCTGCCTCAGGTGACAGT  
█ GGGGCCGGGTGTTGGTCTGTCTGGAAAGACACCAGTTCCGCCCTACCTTCCCTGCCTCCAG  
█ CCCCTATGTCAACCACAGTGGAGGCACATCCTCCAGGAACCTTCCTCATCACAAATGAAA  
█ TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCACGGCCTCATACCAGGAG  
█ GAAGCTGTAACGAAGTTCCCTGAGCTCTAGCCCCCACCTGCCACCATCCAGTTACTTCAATGC  
█ CAGTGGCGTGCCTACCCAGATGTGGCTGCACTTCTGATGGCTACTGGGTGGTCAGCAACA  
█ GAGTGCCATTCCATGGGTGTCGGAACCTCGCCTCTACTCCAGTGGTTGGGGGATCCTA  
█ TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCCCCCCTTGGCTTCTCAACCCAAG  
█ GCTCTACCAGCAGCATGGGCAGGTCTTTGATGTAACCGTGGCTGCCATGAGTCCTGTC  
█ TGGATGAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGATCCTGTAACAGGC  
█ TGGGGAACACCAACTCCCAGTTGCTGAAGACTCTACTCAACCCCTGACCCTTCCATAC  
█ AGGAGAGATGGCTTGTCCCCCTGCCCTGAAGCTGGCAGTTCACTCCCTTATTCTGCCCTGTTG  
█ GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGAGACAGCTTATCTCCCTAACCCCTGAAA  
█ TGCTGTGAGCTTGACTTCAACTCCACCCATGCTCCATCATACTCAGGTCTCCCTACT  
█ CCTGCCCTAGATTCTCAATAAGATGCTGTAACTAGCATTTTGAAATGCCCTCCCTCCGC  
ATCTCATCTTCTCTTCAATCAGGCTTTCAAAGGGTTGTATACAGACTCTGTGACTA  
TTCACTTGATATTCAATTCCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTACTCT  
TTCCTACCCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTCTCAATCTTGTGTTATG  
GCCTTCCATCATAGTTGCCACTCCCTCTCCTACTTAGCTCCAGGTCTTAACCTCTG  
ACTACTCTTGTCTTCCCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCATTG  
TCCATTGAGATTTGCTCTCAGTTACTCATTGCCCCCTGGAACAAATCACTGACA  
TCTACAACCATTACCATCTCACTAAATAAGACTTCTATCCAATAATGATTGATAACCTCAA  
TGTAAAAAA

## **FIGURE 94**

MGLQACLLGLFALILSGKCSYSPEPDQRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS  
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL  
SIRQAELLLPGAEFHYYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGLHRFPPTSSLRQRP  
EPQVTGTVGLHLGVTPSVIRKRYNLTSDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG  
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMAGANISTWVYSSPGRHEGQEPFLQWML  
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLFASGDSGAGCWSVSGRH  
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP  
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG  
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

**Signal sequence:**

amino acids 1-16

□

○

◊

**N-glycosylation site.**

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

□

○

◊

**Glycosaminoglycan attachment site.**

amino acids 361-365, 408-412, 538-542

□

○

◊

**Casein kinase II phosphorylation site.**

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

□

**N-myristoylation site.**

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,  
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,  
521-527, 533-539, 549-555

## FIGURE 95

GCCGCGCGCTCTCTCCGGCGCCCACACCTGTCTGAGCGGCGAGCGAGCCGGCCGGC  
GGGCTGCTCGCGCGGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCCTCTTCCTTCTC  
TTCTTCTGCTCTGTGCTGTGGCAAGTGAGCCCTACAGTGCCCCCTGGAAACCCACTTG  
GCCTGCATACCGCCTCCCTGCGTCTGCCCAAGTCTACCCCTCAATTAGCCAAGCCAGACT  
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCAGTGTCTAAGGGAACCT  
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG  
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCAAAC  
ACCGAGACTCAGGGCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC  
AGGTTCAGCATTGGAGGACTTCCTGCTCAACTACCCCTTCTAACATCAGTGAAGTT  
ATCCACGGGCTGCACCGCACCCCTGGTGGCAGAGAACATGTCCCTCACAGCTGCCACTGCA  
TACACGATGAAAAACCTATGTGAAAGGAACCCAGAAGCTCGAGTGGCTTCTAAAGCCC  
AAGTTAAAGATGGTGGTCGAGGGCCAACGACTCCACTTCAGCCATGCCAGAGCAGATGAA  
ATTCAGTGGATCCGGGTGAAACGCACCCATGTGCCAAGGGTTGGATCAAGGGCAATGCCA  
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACCTCAAAAGCCCCACAAGAGAAAA  
TTTATGAAGATTGGGGTGAGCCCTCCTGCTAACAGCAGTCCAGGCCAGGGCAGAACATTCACTTCTC  
TGGTTATGACAATGACCGACCAGGAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA  
CCTATGACTTGCTCTACCAGCAATGCGATGCCAGCCAGGGCCAGGGCTGGGTCTAT  
GTGAGGATGTGGAAGAGACAGCAGCAGAACATTATTGGCATTGGGCTTCAAGGAGGG  
GCACCAAGTGGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAAATCAGTC  
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGG  
TGACACAGTGTCCCTCCTGGCAGCAATTAAAGGTCTTCATGTTCTTATTTAGGAGAGGCC  
AAATTGTTTGTCTTGCATTGGCGTGCACACGTGTGTGTGTGTGTGTGTGTAAAGGTGT  
CTTATAATCTTACCTATTCTTACAATTGCAAGATGACTGGCTTACTATTGAAAATG  
GTTTGTGTATCATATCATATCATTTAAGCAGTTGAAGGCATACTTTGCATAGAAATAA  
AAAAAAACTGATTGGGCAATGAGGAATATTGACAATTAAAGTTAATCTTCACGTTTGT  
CAAACTTGATTTCATCTGAACATTGTTCAAAGATTATTAATATTAAATATTGGCATA  
CAAGAGATATGAAAAA

## **FIGURE 96**

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLA  
KPDFGAEAKLEVS  
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRD  
SGSSGKS  
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVL  
TAACIHDGKTYVKG  
TQKLRVGFLKPKFKDGGRGANDSTS  
AMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA  
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDV  
KDETYDLLYQQCD  
AQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNV  
AVRITPLKYAQICYW  
IKGNYLDCREG

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 93-97, 207-211

**Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

**Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

**N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

**Serine proteases, trypsin family, histidine active site.**

amino acids 171-177

## FIGURE 97

GCATGCCCTGGGTCTCTGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTTT  
CTGGAGCGCCCCAGCCCTGGGTGGGGCTGTCTCGGCACCTCACCTCCCTGCTGCTGCTG  
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCAGCCTGTGGGAAGCCCCA  
GCAGCTGAACC GGTTGTGGCGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA  
GCATCCAGAAGAATGGGACCCACC ACTGCGCAGGTTCTGCTCACCAAGCCGCTGGGTGATC  
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACTGTTCTGTGCTGCTGGG  
GGCCTGGCAGCTGGGAACCCCTGGCTCTGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC  
CCCACCCCTGTGTATTCTGGAAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG  
CGCTCCATACAGTTCTCAGAGCGGGCCTGCCATCTGCCCTACCTGATGCCCTATCCACCT  
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTGC  
CCCACCCCTCAGACCCTGCAGAACGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT  
CTGTACTGGCGGGAGCAGGACAGGGACCCATCACTGAGGAACATGCTGTGCCGGCTACTT  
GGAGGGGGAGCGGGATGCTTGTCTGGCGACTCCGGGGCCCCCTCATGTGCCAGGTGGACG  
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCAGCGAACAGGCC  
GGGGTCTACATCAGCCTCTGCGCACCGCTCTGGGTGGAGAACGATCGTCAAGGGGTGCA  
GCTCCGGGGCGCCTCAGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCG  
CCGGCGCTCCTAGGGCGCAGCGGACCGGGCTCGGATCTGAAAGGCGGCCAGATCCACA  
TCTGGATCTGGATCTGCGGCGGCCTCGGCGGTTCCCCCGCCGTAAATAGGCTCATCTACC  
TCTACCTCTGGGGGCCGGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCGAC  
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCGCCAACGGCCTCATGTCCCCGCCCCAC  
GACTTCCGGCCCCGCCCCGGGCCCCAGCGCTTTGTATATAATGTTAATGATTATTAT  
AGGTATTTGTAACCCTGCCACATATCTTATTATTCCCTCCAATTCAATAATTATTATT  
CTCCAAAAAAA

## **FIGURE 98**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI PVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAHCFKDNLNKPYLFVLLGAWQLGNPGSRSQKVGVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS
```

**Signal sequence:**

amino acids 1-32

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## **FIGURE 99**

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTCTGATGCTCTGCTGCCGCTACTGCTA  
CTGCTGGTGGCCACCACAGGGCCCGTTGGAGCCCTCACAGATGAGGAGAACGTTGATGGT  
GGAGCTGCACAACCTCTACCGGGCCAGGTATCCCGACGGCCTCAGACATGCTGCACATGA  
GATGGGACGAGGAGCTGGCCGCCTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGCCAC  
AACAAAGGAGCGCGGGCGCCGGCGAGAACTGTTCGCCATCACAGACGAGGGCATGGACGT  
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT  
GCAGCCCAGGCCAGATGTGGCCACTACACGCAGGTGGTATGGCCAAGACAGAGAGGATC  
GGCTGTGGTCCCACCTCTGTGAGAAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT  
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAAGGAGGGACTC  
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC  
CCGGAAGATGCTCAGGATTGCCTTACCTGGTAACTGAGGCCCATCCTCCGGCGACTGA  
AGCATCAGACTCTAGGAAAATGGTACTCCTCTTCCCTAGCAACGGGATTCCGGTTTCT  
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGAAACCCAGGCC  
CCAACTTCCCTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCACCTGCGTAAC  
AACTGAGGTCCCTTCCATTGGCAGCTCACAGCCTGCCCTCCTGGATGAGGAGCCAGTTA  
CCTTCCCCAAATCGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA  
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGCAAG  
GGAACCTCCTACCCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTCCAGTG  
AGGTCTTGGCCTCAGTTTCCAGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC  
CACACGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA  
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCGTCCCTGCCAGGTGCAGAGGCCCTGACA  
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGCCCTGGTCATGTGTGGGCCCTCCCTGGGA  
CTACTGCTCCTGCCTCTGGTGTGGCTGGAATCTTCTGAATGGATACCAACTCAAAGGG  
TGAAGAGGTAGCTGTCCTCTGTCACTTCCCCACCCCTGTCCCCAGGCCCTAAACAAGATA  
CTTCTGGTTAAGGCCCTCCGAAGGGAAAGGCTACGGGCATGTGCCTCATCACACCCTCC  
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC  
GGGCCACACCTCTCCTGCCCTCCCTGAGTCCTGGGGTGGAGGATTGAGGGAGCT  
CACTGCCTACCTGGCCTGGGCTGTCGCCACACAGCATGTGCCTCTCCCTGAGTGCCTG  
TGTAGCTGGGATGGGATTCCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTTC  
TTTGAGTGGGGAGGCAGGGACGGAGGAAAGTAACCTGACTCTCCAATAAAACCT  
GTCCAACCTGTGAAA

## **FIGURE 100**

MHGSCSFLMLLLPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE  
LAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ  
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQC  
PSGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV  
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAHSLPSLDEEPVTFPKS  
THVPIPKSADKVTDKVPSRSPENSMDPKMSLTGARELLPHAQEEAEAEALPPSSEVLAS  
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV  
SGLNSGPGHVWGPLLGLLLPPLVLAGIF

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

 **Glycosaminoglycan attachment site.**

amino acids 439-443

 **Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

 **N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,  
250-256

 **Amidation site.**

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

## **FIGURE 101**

GTAACGTGAGTCAGGCTTTCAATTGGGAAGCCCCCTCAACAGAACCGTCACTTCTCCAAGTTATGGTGGACGT  
ACTTCTGTTCTCCCTCTGCTTACATTAGCAGACCGGACTTAAGTCACAACAGATTATCTTCT  
CAAGGCAAGTCCATGAGCCACCTTCAAAGCCTCGAGAAGTGAACAAACAAATGAATTGGAGACCATCC  
AAATCTGGGACCAAGTCTCGGCAAATATTACACTTCTCTCCTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA  
ACATCTGAAAGAGTTCACTGAAACTTTGACCTTAGCAGCAACAATATTCAGAGCTCCAAACTGCATT  
TCCAGCCCTACAGCTCAAATATCTGTATCTAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTGACAA  
TTTGGCCAACACACTCCTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAAGATGTTAAACT  
GCCCAACTGCAACATCTGAATTGAACCGAAACAAGATTTAGATGGACTGACATTCCAAGGCCTGG  
TGCTCTGAAAGTCTGAAATGCAAAGAAATGGAGTAACGAAACTATGGATGGAGCTTTGGGGCTGAGCAA  
CATGAAATTTGAGCTGGACCATAACAAACCTAACAGAGATTACCAAGGCTGGCTTACGGCTTGCTGATGCT  
GCAGGAACCTCATCTGACCCAAATGCCATAACAGGATCAGCCCTGATGCCCTGGGAGTTCTGCCAGAAGCTCAG  
TGAGCTGGACCTAACCTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTGGCTTAAGCTTACTAAATAC  
ACTGACATTTGGAACAAACAGAGTCAGCTACATTGCTATTGCGCTTCCGGGGCTTCCAGTTAAAGACTTT  
GGATCTGAAAGAACATGAAATTTCTGGACTATTGAAAGACATGAATGGTCTTCTCTGGCTTGACAAACTGAG  
GCGACTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTACTGGTTGGATGCAATTGGAGCA  
TCTAGACCTGAGTGACACGCAATCATGTTACAAGGAATGCAATTTCACAAATGAAGAAACTGCAACAAATT  
GCATTAAATACATCAAGCCTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGGTGGCGAAAACAACCT  
TCAGAGCTTGTAAATGCCAGTTGTGCTGCTTACAGCTGCTAAAGGAAGAAGCATTGGCTGTTAGCCCAGA  
TGGCTTGTGAGTGTGATGATTTCACAGGAGATCACGGTCAGCCAGAACACAGTCGGCAATAAAAGGTT  
CAATTGAGTTCATCTGCTCAGCTGCCAGCAGTGAATTCCCAATGACTTTGCTTGGAAAAAAAGACAATGA  
ACTACTGCATGATGCTGAAATGGAAATTATGCACACCTCCGGGCCAAGGTGGCAGGTGATGGAGTATACCAC  
CATCCTCGGCTGCGCAGGTGGAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCAATCACCTGGTTC  
ATCCTACTCTGTCAGGCAAGCTTACAGTAAATATGCTTCCCTCATTCAACAGACCCCCATGGATCTCACCAT  
CCGAGCTGGGGCATGGCACGCTGGAGTGTGCTGCTGCTGGGGCACCCAGCCCCCAGATGCCCTGGCAGAAGGA  
TGGGGCACAGACTTCCAGCTGCACGGAGAGACGATGCTGATGCCAGGATGACGTGTTCTTATCGT  
GGATGTGAAGATAGAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTGAGCAAATGC  
AACTCTGACTGCTCTAGAAACACCATCATTGGCGCCACTGTTGGACCGAAGTGAACCAAGGGAGAAACAGC  
CGTCTACAGTGCATTGTGGAGGAAGCCCTCCCCCTAAACTGAACCTGGACCAAAGATGATAGCCCATTGGTGGT  
AACCGAGAGGCACTTTGTGAGCAGGCAATCAGCTCTGATTATTGTGGACTCAGATGTCAGTGTGCTGGAA  
ATACACATGTGAGATGTCACACCCCTGGCACTGAGAGAGGAAACGTCAGTGTGATCCCCACTCCAAC  
CTGCGACTCCCCCTCAGATGACACCCCTCGTTAGACGATGACGGATGGCCACTGTTGGGTGTCAGTGTGATCATAGC  
CGTGGTTGTGTTGGGACGTCACTCGTGTGGGTGTCATCATACACACAAAGGCGGAGGAATGAAGA  
TTGCACTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCTAGTTATTGTGTCATCTCAGGGAACGTT  
AGCTGACAGGCAAGGATGGGTACGTGCTTCAAGAAAGTGAAGCCACCAACAGTTGTCACATCTCAGGTGCTGG  
ATTTCCTTACACACATGACAGTAGTGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGAAAGCTGC  
CACAGATCTGTTCTTGTCCGTTTGGGATCCACAGGCCATTGATTTGAAAGGAAATGTGATGGCTCAGA  
TCCTTTGAAACATATCATACAGGTTGCACTGCCAGAACACAGTTTAAATGGACCAACTATGAGCCAGTT  
CATAAAGAAAAGGAGTGCACCCATGTTCTCATCCTCAGAAGAACCTGCCAACGGAGCTTCAGTAATATAC  
GTGGCCTTCACATGTGAGGAAGCTACTAACACTAGTTACTCTCACAAATGAAGGACCTGGAATGAAAATCTGTG  
TCTAAACAAGTCTCTTAAAGTTAGTTAGTGCACATCCAGAGCCAGCGTCGGTGCCTCGAGTAATTCTTCATGGG  
TACCTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGTCAAGC  
AAGAGCCTTTATTGAAAGCTCATTCTCCCCAGACTGGACTCTGGGTCAAGGAGATGGGAAAGAAAGGAC  
AGATTTCAAGGAAAGAACATCAGATTGACCTTAAACAGACTTTAGAAAATACAGGACTCCAAATTTCAAGC  
TTATGACTGGACACATAGACTGAAAGACCAAGGAAAAGCTTAAACATACTACCTCAAGTGAACCTTATT  
AAAGAGAGAGAAATCTTATGTTAAATGGAGTTATGAAATTAAAAGGATAAAATGCTTATTATACAGAT  
GAACCAAAATTACAAAAAGTTATGAAAATTAAACTGGGAATGATGCTCATATAAGAATACCTTTAAACTA  
TTTTTAAACTTGTGTTATGCAAAAAGTATCTTACGAAATTAAATGATATAAATCATGATTATTGTATT  
TTATAATGCCAGATTCTTTATGAAAATGAGTTACTAAAGCATTAAATAACCTGCCATTGACCAATT  
TTAAATAGAAGTTACTTCATTATATTGCACTTAAATAAAATGTGCAATTGAA

## **FIGURE 102**

MVDVLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQLSLREVKLNNELETIPNLGPVSAN  
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP  
GYFDNLANTLLVLKLNRRNRIASAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKM  
QRNGVTKLMGDGFWGSLSNMEILQLDHNNLTEITKGWLGYLLMLQELHLSQNAINRISPDAWE  
FCQKLSLELDLTFNHLRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLDDLKNNE  
ISWTIEDMNGAFSGLDKLRRRILQGNRIRSITKKAFTGDALEHLDLSDNAIMSLQGNAFSQ  
MKKLQQLHLNTSSLLCDCQLKWLWPQWAENNQSFVNASCAPQLLKGRSIFAVSPDGFVCD  
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQG  
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVAKLTNVMLPSFTKTPMDLTIRAGA  
MARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCAQN  
SAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPQLNWTKDDSPLVVTER  
HFFAAGNQLLIVDSDVSDAGKYTCMSNTLGERGNVRLSVIPTPTCDSPQMTAPSLEDDG  
WATVGVIIIAVVCCVVGTSLVWVVIYHTRRNEDCSITNTDETNLPADIPSYLSSQGTLAD  
RQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEATDLCFLCPFLGSTGP  
MYLKGNVYGSDFETYHTGCPDPRTVLMHYEPSYIKKKECYPCHPSEESCERSFSNISW  
PSHVRKLLNTSYSHNEPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA  
YSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQS  
YDLDT

 **Signal sequence:**

 amino acids 1-19

 **Transmembrane domain:**

 amino acids 746-765

 **N-glycosylation site.**

 amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

 **Glycosaminoglycan attachment site.**

 amino acids 826-830

 **Casein kinase II phosphorylation site.**

 amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

 **Tyrosine kinase phosphorylation site.**

 amino acids 607-615

 **N-myristylation site.**

 amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTGTTGGGTGCCTTGCAAAAATG  
AAGGATGCAGGACGCAGCTTCTCTGGAACCGAACGCAATGGATAAAACTGATTGTGCAAGAGAGAAGGAAGAAC  
GAAGCTTTCTGTGAGCCCTGGATCTAACACAAATGTGTATATGTGACACAGGGAGCATTCAAGAATGAAA  
TAAACCAGAGTTAGACCCGCGGGGTTGGTGTGTTCTGACATAAATAATCTTAAAGCAGCTGTTCCCCTCC  
CCACCCCCAAAAAAAGGATGATTGGAATGAAGAACCGAGGATTCAAAGAAAAAGTATGTTCACTTCTC  
TATAAAGGAGAAAGTGAAGCAAGGAGATATTGGATGAAAGTAAAGTTGGGCTTTTAGTAAAGTAAAGAAC  
GGTGTGGTGGTGTCTTCTTGAATTCCCACAAAGAGGAGAGGAAATTAAATAACATCTGAAAGAAA  
TTTCAGAGAAGAAAAGTTGACCGCGGAGATTGAGGCATTGATTGGGGAGAGAACACCAGCAGAGCACAGTTGA  
TTTGTGCCATGTTGACTAAATTGACGGATAATTGCAAGTGGATTCTTCATCAAACCTCCTTTAAAT  
TTTATTCTCTTGGTATCAAGATCATCGCTTCTCTGTTCTAACACCTGGATTTCATCTGGATGTTGCT  
GTGATCAGTCTGAAATACAACGTGTTGAATTCCAGAACAGGACCAACACCAGATAAATTATGAATGTTGAACAAGAT  
GACCTTACATCCACAGCAGATAATGATAGGTCCTAGGTTAACAGGGCCATTGACCCCTGCTGTGGTCT  
GCTGGCTCTTCAACTTCTGTGGTGGCTGGCTGGTGGGGCTCAGACCTGCCCTCTGTGTGCTCTGCAGCAA  
CCAGTTCAGCAAGGTGATTGTGTTGGAAAAACCTCGCTGGATGGCATCTCCACCAAACACAGGCT  
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTCAAGCACTTGAGGCACTTGGAAATCCT  
ACAGTTGAGTAGGAACCATATCAGAACCAATTGAAATTGGGGCTTCAATGGTCTGGCAACCTCAACACTCTGGA  
ACTCTTGACAATCGTCTACTACCATCCGAATGGAGCTTGTATACTTGTCTAAACTGAAGGAGCTCTGGTT  
GCGAAACAACCCATTGAAAGCATCCCTTATGCTTTAACAGAATTCCCTTGCCTGACTAGACTTAGG  
GGAATTGAAAAGACTTCATACATCTCAGAAGGTGCCTTGAAGGTCTGCAACTTGAGGTATTGAACCTTGC  
CATGTGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAAACTAGATGAGCTGGATCTTCTGGGAAATCA  
TTTATCTGCCATCAGGCCTGGCTTTCCAGGGTTGATGCACCTCAAAACTGTGGATGATACAGTCCCAGAT  
TCAAGTGATTGAACGGAATGCCTTGACAACCTTCAGTCAGTCACTAGGGAGATCAACCTGGCACACAATAATCTAAC  
ATTACTGCCTCATGACCTTCACTCCCTGCATCATCTAGAGCGGATACATTACATCACAACCCCTGGAACTG  
TAACGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTGAAACACAGCTGTTGTGCCGGTG  
TAACACTCCTCCAATCTAAAGGGAGGTACATTGGAGAGCTGACCAGAAATTACTCACATGCTATGCTCCGGT  
GATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAGGCATGGCAGCTGAGCTGAAATGTCGGCCTCCACATC  
CCTGACATCTGTATCTGGATTACTCCAAATGGAACAGTCAGTGCACATGGGGCGTACAAAGTGCAGATAGCTGT  
GCTCAGTGTGTTGGTACGTTAAATTTCACAAATGTAACCTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA  
TTCCCTTGGAAACTACTGTGTTCAAGCCACCTGAATGTTACTGCAGCAACCAACTACTCTTCTTACTTTTCA  
AACCGTCACAGTAGAGACTATGGAGACCACTGGGACCTCTCAGGATGAGGACGGACGACAGATAACATGTGGTCCCACTCC  
AGTGGTCGACTGGGAGACCAATGTCAGGATGACCCAGGAAATTGATGAGGTCTGAAGACTACAAAATCATCAT  
CACCACCCAGTGACTIONTAAACAGTGGATCCCAGGAAATTGATGAGGTCTGAAGACTACAAAATCATCAT  
TGGGTGTTTGTGGCATCACACTCATGGCTGCAGTGTGCTGGTCTTACAAGATGAGGAAGCAGCACCA  
TCGGCAAAACCATCACGCCAACAGGACTGTTGAAATTATTAAATGTGGATGATGAGATTACGGGAGACACACC  
CATGGAAAGCCACCTGCCATGCCCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATCAAATCTCCCTT  
CAACCACACAAACAGTTAACACAATAATTCAATACACAGTTCACTGCATGAACCGTTATTGATCCGAATGAA  
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTACAGAGTTACAAAAACAAACAAATCAAAAAAA  
GACAGTTATTAAAAATGACACAAATGACTGGCTAAATCTACTGTTCAAAAGTGTCTTACAAAAACAA  
AAAAGAAAAGAAATTATTATTAAACATTCTATTGTGATCTAAAGCAGACAAAAA

## FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPLSLRRLDGELKRLS  
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWCNC  
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLN  
TEGMAAE LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTN  
TVQDTGMYTCMVNSVGN TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVG  
PPTVVDWETTNVTTSLTPQ STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFV  
AITLMAAVMLVIFYKMRKQHHRQN HHAPTRTVEIINV  
DDEITGDTPMESHLPMPAIEHEHLNHNSYKSPFNHTTVNTINSIHSS  
VHEPLLIRMN  
SKDNVQETQI

- █ **Signal sequence:**  
█ amino acids 1-44
- █
- █ **Transmembrane domain:**  
█ amino acids 523-543
- █
- █ **N-glycosylation site.**  
█ amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,  
█ 442-446, 488-492, 606-610
- █
- █ **cAMP- and cGMP-dependent protein kinase phosphorylation site.**  
█ amino acids 183-187
- █
- █ **Casein kinase II phosphorylation site.**  
█ amino acids 268-272, 417-421, 465-469, 579-583, 620-624
- █
- █ **N-myristoylation site.**  
█ amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
█ 391-397, 422-428, 433-439, 531-537

## **FIGURE 105**

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTGGGTTCCCTCTGCTGTTGGGGCA  
TGAAAGGGCTTCGCCGCCGGAGTAAAAGAAGGAATTGACCGGGCAGCGCAGGGAGGAGCGCAGCGACCGC  
GAGGGCGGGCGTGCACCTCGGCTGGAAGTTGTGCCGGGCCCCGAGCGCGCAGCGCAGGGCTGGAGCTCGGGTAGA  
GACCTAGGCCGCTGGACCAGGATGAGCGCAGGCCGCTCCGTGCGCGCAGCGCAGGGCTGGAGCTGCTGTC  
GCGGTGCTGGGGCGCTGGCGCTGCCGCTGGACAGCGGGCGTGCAGGGAACTCGGGCAGCCCTCTGGGGTAGCGC  
GAGCGCCCATGCCCAACTACCTGCGCTGCCCGGGACCTGCTGGACTGAGCTGTAAGCGGCTAGCGCTT  
CCGAGCCACTCCGCTGGGTGCGCTGGACTTAAGTCACAAACAGATTATCTTCATCAAGGCAAGTTC  
ATGAGCCACCTTCAAAGCCTCGAGAAGTGAACAAACATGAATTGGAGACCATTCAAATCTGGGACCA  
GTCTCGGCAAATATTACACTCTCTCCTGGCTGGAAACAGGATTGTTGAATACTCCCTGAACATCTGAAAGAG  
TTTCAGTCCCTGAAACCTTGGACCTTAGCAGGAACAATATTTCAGAGCTCCAAACTGCATTCCAGCCCTACAG  
CTCAAATATCTGTATCTCAACAGCAACCAGTACATCAATGGAACCTGGTATTTGACAATTGGCCAACACA  
CTCCTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCAAAGATGTTAAACTGCCCAACTGCAA  
CATCTGAATTGAAACGAAACAAGATAAAAATGTAGATGGACTGACATTCCAAGGGCTTGGTCTGAGTCT  
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGCTGAGCAACATGGAATTTTG  
CAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGTGATGCTGAGGAACCTCAT  
CTCAGCCAAATGCCATCACAGGATCAGCCCTGATGCCCTGGAGTCTGCCAGAAGCTCAGTGAGCTGGACCTA  
ACTTTCAATCACTTCAAGGTTAGATGATTCAAGCTTCCCTGGCCTAAGCTTACTAAATACACTGCACATTGGG  
AAACAACAGAGTCAGCTACATTGCTGATTGTGCCCTCCGGGGCTTCCAGTTAAAGACTTTGGATCTGAAAGAAC  
AATGAAATTCTCGGACTATTGAAGACATGAATGGTCTTCTCTGGGCTTGACAAACTGAGGCGACTGATACTC  
CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTCACTGGTTGGATGCACTGGAGCATCTAGACCTGAGT  
GACAACGCAATCATGTTTACAAGGCAATTGCAATTTCACAAATGAAAGAAACTGCAACAAATTGCAATTAAATACA  
TCAAGCCTTTGTGCGATTGCCAGCTAAATGGCTCCCACAGTGGTGGCGAAAACAAACTTCAAGGCTTGTG  
AATGCCAGTTGTGCCCATCCTCAGCTCTAAAGGAAGAAGCATTTTGCTGTTAGCCAGATGGCTTGTG  
GATGATTTCCAAACCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTGAGTT  
ATCTGCTCAGCTGCCAGCAGTGAATTCCCAATGACTTTGCTGGAAAAAAAGACAATGAAACTACTGCATGAT  
GCTGAAATGAAAATTATGACACACCTCCGGGCCAAGGTGGCAGGTGATGGAGTATACCAACATCCTTCGGCTG  
CGCAGGTTGAAATTGCCAGTGGGGAAATATCAGTGTGTCATCTCAACTTTGGTCACTCCTACTCTGTC  
AAAGCCAAGCTTACAGTAAATATGCTCCCTCATCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGCC  
ATGGCACGCTGGAGTGTGCTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGGGCACAGAC  
TTCCAGCTGCACGGAGAGACGCATGCACTGATGCCAGGGATGACGTGTTTATCGTGGATGTGAAGATA  
GAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTCAGCAAATGCAACTCTGACTGTC  
CTAGAACACCATCATTTCGCGGCCACTGTTGACCGAATGTAACCAAGGGAGAACAGCCGCTTACAGTGC  
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAGATGATAGCCATTGGTGGTAACCAGAGGGCAC  
TTTTTGCAGCAGGCAATCAGCTCTGATTATTGTGGACTCAGATGTCAGTGATGCTGGAAATACACATGTGAG  
ATGTCTAACACCCCTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCACCTCAACCTGCACCTCC  
CAGATGACAGCCCCATCGTAGACGATGACGGATGGGCCACTGTTGGGTGTCGTGATCATAGCCGTGGTTGCTGT  
GTGGTGGGCCAGTCACTCGTGTGGGTGGTCATCATATACACACACAAGGGAGGAATGAAGATTGAGCATTAC  
AACACAGATGAGACCAACTTGCAGCAGATATTCTAGTTATTGTGATCTCAGGGAACTGTTAGCTGACAGGAG  
GATGGGTACGTGCTTCAGAAAAGTGGAAAGCACCACAGGTTGTCACATCTTCAGGTGCTGGATTTTCTTACCA  
CAACATGACAGTGTGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTT  
CTTTGTCGTTTGGATCCACAGGGCTTATGTTGAAGGGAAATGTGATGGCTCAGATCCTTTGAAACAA  
TATCATACAGGTTGCACTGCCAGGCAACAGTTTAATGGACCACTATGAGCCAGTTACATAAAAGAAAAAG  
GAGTGTACCCATGTTCTCATCCTTCAGAAGAATCCTGCAACGGAGCTTCAGTAATATATCGTGGCCTTCACAT  
GTGAGGAAGCTACTAACACTAGTTACTCTCACAAATGAAGGACCTGGAAATGAAAATCTGTCTAAACAAAGTCC  
TCTTTAGATTGAGTGCACATCCAGAGCCAGCGTGGCTCGAGTAATTCTTCAGGGTACCTTGGAAAA  
GCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGGCCATCAGATTGTCAGGCCAGAGGCC  
TTGAAAGCTCATTCTCCCCAGACTTGGACTCTGGTCAGAGGAAGATGGAAAGAAAGGACAGATTTCAAGGAA  
GAAAATCACATTGTACCTTAAACAGACTTTAGAAAACAGACTACAGGACTCCAAATTTCAGTCTTATGACTTGGAC  
ACATAGACTGAATGAGACCAAGGAAAGCTTAAACATACACCTCAAGTGAACCTTTATTAAAGAGAGAGAAT  
CTTATGTTTTAAATGGAGTTATGAAATTAAAAGGATAAAATGCTTATTATACAGATGAACCAAAATTAC  
AAAAAGTTATGAAAATTTATACTGGGAATGATGCTCATATAAGAATACCTTTAAACTATTGTTAACTTTG  
TTTATGCAAAAAGTACTTACGTTAAATTATGATATAAATCATGATTATTATGTTATGTTATAATGCCAGA  
TTCTTTTATGGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTACCATTTAAATAGAAGT  
ACTCATTATATTGCACTTATTTAAATAAAATGTCATTGAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 106

MSAPSLRARAAGLGLLCAVLGRAGRSDSGGRGELGQPSGVAERPCPTTCRCLGDLDCSR  
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSANIT  
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLQLNSNRVTSMEPGY  
FDNLANTLLVLKLNRRNRISSAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQR  
NGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC  
QKLSLEDDLTNFNHLRSRLDDSSFLGLSILLNTLHIGNNRVSYIADCAFRLGSSLKTLNNEIS  
WTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK  
KLQLQHLNTSSLCDCKWLQPQWVAENNQSFVNASCAPQLLKGRSIFAVSPDGVCDDF  
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQGGE  
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYVAKLTVNMLPSFTKTPMDLTIRAGAMA  
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA  
GSISANATLTVLETPSFLRPLLRTVTKGETAVLQCIAGGSPPPKNWTKDDSPLVVTERHF  
FAAGNQLLIIVDSDVSDAGKYTCMSNTLTERGNVRLSVIPTPTCDSPQMTAPSLLDDGWA  
TVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTLADRO  
DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY  
LKGNVYGSDPFETYHTGSPDPRTVLMHDYEPSYIKKKECYPCHPSEESCRSFSNISWPS  
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS  
SFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICFKQTLENYRTPNFQSYDLDT

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 808-828

**N-glycosylation site.**

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

**Glycosaminoglycan attachment site.**

amino acids 886-890

**Casein kinase II phosphorylation site.**

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

**Tyrosine kinase phosphorylation site.**

amino acids 667-675

**N-myristoylation site.**

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

**Leucine zipper pattern.**

amino acids 58-80, 65-87

## **FIGURE 107**

CAAAACTTGCCTCGCGGAGACGCCAGCTGACTTGAATGGAAGGAGCCCAGGCCGGAGCGCAGCTGAGAC  
TGGGGGAGCGCTTCGGCCTGTGGGCGCCGCTCGGCCGGGGCGCAGCAGGAAGGGAGCTGTGGTCTGCC  
CTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGAGCCCTGGTGGTCCCGTCCCTATCCCTCTTATATA  
GAAACCTTCCACACTGGGAAGGCAGCGGAGGGCTCATGGTGAGCAAGGAGGCCGCTGATCTGAG  
GCGCACAGCATTGGAGTTACAGATTTACAGATACCAAATGGAAGGCGAGGAGGCAGAACAGCCTGCC  
TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGGCACCCCTGCAGGCACATGGCCAGAGGCCGGTGTGC  
TGCTCCTGCTGCTGCTGCCACAGCTGCACCTGGGACCTGTGCTTGCGTGAGGGCCCAAGGATTGGCCGAA  
GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTGCGGAGGGAGGCCGTGCTGTACTGAGCCCTGAGG  
AGCCCGGGCTGGCCAGCCGGTCAGCTGCCCGAGACTGTGCTGTTCCAGGAGGGCGTCGGACTGTG  
GCGGATTGACCTGCGTGAGAGTTCGGGGGACCTGCTGAGCACACCAACCACTATCTGCAGAACACCAGC  
TGGAAAGATCTACCCCTGAGGAGCTCCCGGCTGCACCCGGCTGGAGAGACTGAACCTGCAAAACAAACCGCCTGA  
CTTCCCAGGGCTCCAGAGAACGGCTTGAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAAGC  
TGACCTTGGCACCCGCTTCCCTGCCAAACGCCCTGATCAGTGGACTTGTGTCCCAACATCTCACCAAGATCT  
ATGGGCTCACCTTGGCAGAACGCAAACTTGAGGTCTGTGACCTGCAACAAACAGCTGGCAGACGCCGGC  
TGCCGGACACATGTTCAACGGCTCAGCAACGCTCAGGCTCTCATCCTGTCAGCAACTTCTGCCACGTGC  
CCAAGCACCTGCCGCTGCCCTGTACAAGCTGCACCTCAAGAACAAACAGCTGGAGAAGATCCCCGGGGCCT  
TCAGCGAGCTGAGCAGCTGCGAGCTATACTGCAGAACAAACTACCTGACTGACGAGGGCTGGACACGAGA  
CCTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCAGCAACACCTGTCGGTCCAGCTGGCTGC  
CGCGCAGCCTGGTGTGCTGCACTTGGAGAAGAACGCCATCCGGAGCGTGGACGCGAATGTGCTGACCCCCATCC  
GCAGCCTGGAGTACCTGCTGTCACAGCAACCAGCTGCCGGAGCAGGGCATCCACCAACTGGCCTTCCAGGGCC  
TCAAGCGGTTGACACGGTGCACCTGTACAACACCGCTGGAGGCCGTGCCAGTGGCCTGCCACGTGGAGTGC  
GCACCCCTCATGATCCTGCACAACCAGATCACAGGCAATTGGCGCGAAGACTTGGCACCACCTACTCCTGGAGG  
AGCTCAACCTCAGCTACAACCGCATCACAGGCCACAGGTGCACCGCAGCCTCCGCAAGCTGCCCTGCTGC  
GCTCGCTGGACCTGTGGCAACCCTGTCACACGCTGCCACCTGGCTGCCATGGCTGAAATGTCCATGTGCTGAAGG  
TCAAGCGCAATGAGCTGGCTGCCATTGGCACAGAGGGCGCTGGCGGGCATGGCTCAGTGCGTGAGCTGACCTCA  
CCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCGTGCCTGGTGGACCTGCCCATCTGCAGCTGCTGGACA  
TCGCCGGGAATCAGCTCACAGAGATCCCCGAGGGCTCCCCGAGTCACTTGAGTACCTGCAGAACAAACA  
AGATTAGTGGCTGCCGCAATGCTTCGACTCCACGCCAACCTCAAGGGATCTTCTCAGGTTAACAAAGC  
TGGCTGTGGGCTCCGGTGGACAGTGCCTTCCGGAGGCTGAAGCACCTGCAGGTCTTGACATTGAAGGCAACT  
TAGAGTTGGTGACATTCCAAAGGAGCGTGGCCCTTGGGAAGGAAAGGAGGAGGAGGAGGAGGAGGAGG  
AGGAAGAGGAAACAAAGATAGTGACAAGGTGATGCAGGTGCAGATGTGACCTAGGATGATGGACCCGGACTTTCTGC  
AGCACACGCCCTGTGTGCTGAGCCCCCCACTGCCGTGTCACACAGACACCCAGCTGCACACATGAGGCA  
TCCCACATGACACGGCTGACACAGCTCATATCCCCACCCCTCCACGGCGTGTCCCACGCCAGACACATGC  
ACACACATCACACCCCTAAACACCCAGCTGCCACACACAACTACCCCTCAAACACCACACAGTCTGTCACAC  
CCCCACTACCGCTGCCACGCCCTGTAATCATGCAGGGAGGGCTGCCCTGGCACACACAGGCCAC  
TTCCCTCCCCCTGCTGACATGTGATGCGTATGCCATACACACCACACACATGCACAGTCGTGCGAA  
CAGCCCTCCAAAGCTATGCCACAGACAGCTTGGCCAGCAGAATGCCATAGCAGCTGCCGTGCC  
GTCCATCTGCCGTCCGTTCCCTGGAGAAGACACAAGGGTATCCATGCTGTGGCCAGGTGCCACCC  
GGAACTCACAAAGCTGGTTTATCCTTCCATCCTATGGGACAGGCCTCAGGACTGCTGCCCTGGCC  
TGGCCACCCCTGCTCCTCCAGGTGCTGGCAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA  
CAGGCACTTTCCAATGGCAAGCCAGTGGAGGCAGGATGGAGAGGCCGGCTGGTGTGCTGGGGCCTGGGG  
CAGGAGTGAAGCAGAGGTGATGGGCTGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTT  
GTTCTCAGGCCTGTGGGGAGTCCGGGTGCCTTTATTTTATCTTCTAAGGAAAAAAATGATAAAAT  
CTCAAAGCTGATTTCTTGTATAGAAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAAA

## **FIGURE 108**

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS  
GGHSLSPPEENEFAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLP  
EHTNHLSLQNNQLEKIYPEELSRLHRLETNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNK  
LTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV  
EVLILSSNFLRHPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN  
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSDANVLTPIRSLEYLLLHSN  
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPDRVRLMILHNQITGIGREDFATTYF  
LEELNLSYNRITSQVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEALAALA  
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL  
QNNKISAVPANAFDSTPNLKIGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD  
RGRLGKEKEEEEEEEEEEETR

- █ **Signal sequence:**  
█ amino acids 1-48
- █ **N-glycosylation site.**  
█ amino acids 243-247, 310-314, 328-332, 439-443
- █ **Casein kinase II phosphorylation site.**  
█ amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595
- █ **N-myristoylation site.**  
█ amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554
- █ **Leucine zipper pattern.**  
█ amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

## FIGURE 109

GGGAGGGGGCTCCGGGCGCCGCGCAGCAGACCTGCTCCGGCGCGCTGCCGCTGCTCTCCGGGAGCGGCAG  
CAGTAGCCGGCGGCAGGGCTGGGGTCTCGAGACTCTCAGAGGGCGCTCCCATGGCGCCACCACCC  
CAACCTGTTCTCGCGGCCACTGCGCTGCCAGGACCCGCTGCCAACATGGATTCTCTGGCGTGGT  
GCTGGTATCCTCGCTCTACCTGCAGGCGGCCGAGTCAGCGGAGGTGGCCAGGCAAATAGTGTATCGAT  
TGGCTATGCTTATGGGAGGATTGACTGCTGCTGGGCTGCCAGTCTGGGACAGTGTAGCC  
TGTGTGCCAACACGATGCAAACATGGTAATGTATCGGCCAAACAAGTCAAGTGTACATCCTGGTTATGCTGG  
AAAACCTGTAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCAGGCCCTGTAAGCACAGGTGATGAACACTTA  
CGGCAGCTACAAGTGTACTGCTCAACGGATATATGCTCATGCCGATGGTCTCTGCTCAAGTGCCCTGACCTG  
CTCCATGGCAACTGTCAGTATGGCTGTGATGTTAAAGGACAAATACGGGCCAGTGCCATCCCTGGCCT  
GCACCTGGCTCTGATGGGAGGACCTGTTGAGATGTTGATGAAATGTGCTACAGGAAGGCCCTGCCCTAGATT  
TAGGCAATGTCACACTTTGGGAGGCTACATGTCAGTGTCACTGGTCACTGTCAGTGTATATTGGAGG  
CAAATCAATGTCATGACATAGACGAATGTCACGGTCACTGTCAGTGTCACTGTCAGCAGCTTGCTCGATGTTAA  
CGTAGTGGTCTACAAGTGCACAGGATACAGGGTGTGGACTGACTTGTGTATATCCAAA  
AGTTATGATTGAAACCTCAGGTCCAATTGTCACAAAGGGAAATGGTACCATTTAAAGGGTACACAGGAAA  
TAATAATTGGATTCTGATGTTGAAAGTACTTGGCTCCGAAGACACCATATATTCCCTATCATTACCAA  
CAGGCCTACTCTAAGCAACAAGACCTACACCAAGCCAACCCAATTCTACTCCACCAACCCACCA  
CCTGCCAACAGAGCTCAGAACACCTTACACCTACACCCAGAAAGGCCAACCAACGGACTGACAACATAGC  
ACCAGCTGCCAGTACACCTCAGGGGATTACAGTTGACAACAGGGTACAGACAGACCCCTGAAACCCAGAGG  
AGATGTGTCAGTGTCTGGTACACAGTTGTAATTGGACATGGACTTGTGGATGGATCAGGGAGAAAGACAA  
TGACTTGCACTGGAACCAATCAGGGACCCAGCAGGTGACAATATCTGACAGTGTGGCAGCAAAGCCCCAGG  
GGGAAAAGCTGCACGCTGGTGTACCTCTGGCCCTCATGCATTAGGGACCTGTGCCTGTCATTAGGCA  
CAAGGTGACGGGCTGCACTCTGGCACACTCCAGGTGTTGTGAGAAAACAGGTGCCACGGAGCAGCCCTGTG  
GGGAAGAAATGGTGGCCATGGCTGGAGGCAAACACAGATCACCTTGCAGGGGCTGACATCAAGAGCGAATCACA  
**AAGATGATTAAGGGTTGGAAAAAAAGATCTATGATGGAAATTAAAGGAACTGGATTATTGAGCCTGGAGAAG**  
AGAAGACTGAGGGCAAACCAATTGATGGTTTCAAGTATATGAAGGGTGGCACAGAGAGGGTGGCACCAGCTG  
TTCTCCATATGCACTAAGAATAGAACAGAGGAAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTGGCAGG  
GCCATTGTTAGAATACTCTATAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTCTCTTCTAAAAATTAGA  
TAAAATTGCTTATTAAGATGGTAAAGATGTTCTACCAAGGAAAGTAACAAATTATAGAATTCCAAA  
AGATGTTGATCCTACTAGTAGTGTGAAATCTTGAACATAATAATTGGACAAGGCTTAATTAGG  
CATTTCCCTTGTGACCTCTAAATGGAGAGGGATTGAAAGGGGAGAGGCCACCAAATGCTGAGCTCACTGAAATA  
TCTCTCCCTTATGGCAATCTTAGCAGTATTAAGAAAAAGGAAACTATTATCCAAATGAGAGTATGATGGAC  
AGATATTGTTAGTATCTCAGTAATGTCCTAGTGTGGCGGTGGTTCAATGTTCTCATGGTAAAGGTATAAGCC  
TTTCATTGTCATGGATGATGTTCAAGATTGGCTTCAAGGAAACAGTTCAAGGAGAG  
ATTTCATGGGTGCAATTCTCTCTGCTCGTGTGACAAGTTATCTGGCTGCTGAGAAAGAGTGCCCTGG  
ACACCCGGCAGACCTTCTTCACTCATCAGTATGATTGATTCTCTTATCAATTGGACTCTCCAGGTTCCAC  
AGAACAGTAATATTTTGAAACAATAGGTACAATAGAAGGTCTCTGTCATTAAACCTGTAAGGGCTGG  
AGGGGAAAATAATCATTAAGCCTTGAGTAACGGCAGAATATATGGCTGAGATCCATTAAATGGTTCATT  
TCCTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGAAAATAATGAAAATTACTTTCGATGCCAA  
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTGTTTATTATTAATGTTT  
CTAAAATAAAATGTTAGTGGTTTCCAAATGGCTAATAAAAACAATTATGTAATAAAACACTGTTAGTAAT

## **FIGURE 110**

MDFLLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP  
RCKHGECIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD  
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDGRTCDVDECATGRASCPRFRQC  
VNTFGSYICKCHKGFDLMIYIGGKYQCHDIDECSLGQYQCSSFARCYNVRSYKCKCKEGYQG  
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNWIPDVGSTWWPPKTPYIPPIITNRP  
TSKPTTRPTPKPTPIPTPPPPPPTELRTPLPPTPERPTTGLTTIAPAASSTPPGGITVDN  
RVQTDPQKPRGDVFSQLVHSCNFDHGLCGWIKEKDNDLHWEPIRDAGGQYLTVA  
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI  
TLRGADIKSESQR

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 273-277

**Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

**Tyrosine kinase phosphorylation site.**

amino acids 199-206

**N-myristoylation site.**

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,  
421-427, 433-439, 462-468, 476-482

**Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

**Cell attachment sequence.**

amino acids 382-385

**EGF-like domain cysteine pattern signature.**

amino acids 75-87

## **FIGURE 111**

CTTCTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTGCCCTTAGATTGTGA  
AATGTGGCTCAAGGTCTTCACAACTTCCCTTGCACAGGTGCTGCTGGGGCTGA  
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTACCTACCGTC  
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCA  
ACAATGCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTCTGACTTGAATACC  
AACACAAGTCACCATGATGCCACCCAATGCATCTGCTTATCAACCCACTGCAGTCCCT  
GATGAAGGCAATTACATCGTGAAGGTCAACATTCAAGGAAATGGAACATCTATCTGCCAGTCA  
GAAGATAACAAGTCACGGTTGATGATCCTGTACAAAGCCAGTGGTCAGATTCACTCCCT  
CTGGGGCTGTGGAGTATGTGGGAACATGACCCCTGACATGCCATGTGGAAGGGGCACTCGG  
CTAGCTTACCAATGGCTAAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTC  
TCCCCAAAACAATACCCCTCATATTGCTCAGTAACCAAGGAAGACATTGGGAATTACAGCT  
GCCTGGTGAGGAACCCCTGTCAGTGAATGGAAAGTGTATCATTATGCCCATCATATTAT  
GGACCTTATGGACTTCAAGTGAATTCTGATAAAAGGGCTAAAGTAGGGGAAGTGTACTGT  
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT  
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAAGCATGGGCCTCGCTTAGAAGTT  
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGCTTACAACAACATAAC  
CGGCAGGCAAGATGAAACTCATTCACAGTTACATCACTCCGTAGGACTGGAGAAGCTG  
CACAGAAAGGAAATCATTGTCACCTTCAAGTATAACTGAATATCACTATTGGATT  
ATATCCATGTGCTTCTCTTCCATGGAAAAAAATCAACCCCTACAAAGTTATAAAACAGAA  
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG  
CTCTGGATGACTTCGGAATATATGAATTGTTGCTTCCAGATGTTCTGGTGTTCAGG  
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATGGGCAAGATTGCACAGTACAGT  
GTATGAAGTTATTCAAGCACATCCCTGCCAGCAGCAAGACCATTCCAGAGTGAACTTCA  
GCTAACAGTACATTGAGTGAAGAAATTCTGAAGAAACATTAAAGGAAAACAGTGGAAAAGT  
ATATTAAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTACTCATTATTCC  
TGCAGAATAGAGGCATTATGCAAATTGAAGTGCAGGTTTCAGCATATA  
GTGCAACAGAAAAACATGTTGGGAAATATTCCCTCAGTGGAGAGTCGTTCTCATGCTGACGG  
GGAGAACGAAAGTGACAGGGGTTCCCTCATAAGTTGTATGAAATATCT  
ACAAACCTCA  
ATTAGTTCTACTCTACACTTCACTATCAACACTGAGACTATCCTGCTCACCTACAAA  
TGTGGAAACTTACATTGTTGATTTTCAGCAGACTTGTGTTTATTAAATT  
TTAGTG  
TTAAGAATGCTAAATTATGTTCAATTTCAGGAAATTTCTATCTTGTATTGTACAA  
CAAAGTAATAAGGATGGTTGTCAACAAAACAAA  
ACTATGCCTCTCTTTTTCAATCACC  
AGTAGTATTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATT  
TTTTTTCAAGGAAAGATGGATTCAAATAATTATTCTGTTTGCTTTAAAAAAA  
AAAAAAA

## **FIGURE 112**

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH  
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGTLSASQ  
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS  
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV  
DLGEAILFDCSADSHPPNTYSWIRTDNTTYIIKHGPRLEVASEKVAQKMDYVCCAYNNIT  
GRQDETHFTVIITSVGLEKLAQKGKSLSPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK  
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSPASDCVSGQDLHSTV  
YEVIQHIPAQQQDHPE

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 341-359

**N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

**Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

**Tyrosine kinase phosphorylation site.**

amino acids 272-280

**N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 113**

GCAAGCGCGAAATGGCGCCCTCCGGGAGTCTGCAGTTCCCCTGGCAGTCCTGGTGTGTT  
GCTTGGGGTGTCTCCCTGGACGCACGGCGGGAGCAACGTTCGCGTCATCACGGACGAGA  
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTATGCCCCGTGGTGCCTGCT  
TGTCAAAATCTCAACCGGAATGGGAAAGTTGCTGAATGGGAGAAGATCTTGAGGTTAA  
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC  
TTCCTACTATTTATCATTGAAAGATGGTGAATTAGGCGCTATCAGGGTCCAAGGACTAAG  
AAGGACTTCATAAAACTTATAAGTGATAAAAGAGTGGAAAGAGTATTGAGCCGTTCATCATG  
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTTTCAGCTATCTATGTGGA  
TCAGGACGTGCCATAACTACTTATTGAAAGACCTGGATTGCCAGTGTGGGATCATATACT  
GTTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGCG  
AGATTGCCTTGTCCTCAAAAAGGCGCAGACCAACAGCCATACCCATACCCCTCAAAAAAAT  
TATTATCAGAACTGCACAAACCTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA  
GATGTTCAGAAGAAGAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAATGC  
CATAAAGACAACGCTCTGGGTCCATCATTGCCACAGATAAATCCTAGTTAAATTATAG  
TTATCTTAATATTATGATTTGATAAAACAGAAGATTGATCATTTGTTGGTTGAAGTG  
AACTGTGACTTTTGAATATTGCAGGGTTCAGTCTAGATTGTCAATTAAATTGAAGAGTCTA  
CATTCAGAACATAAAAGCACTAGGTATACAAGTTGAAATATGATTTAACAGTATGATG  
GTTAAATAGTTCTAATTGGAAAAATCGGCCAAGCAATAAGATTATGTATATTGT  
TTAATAATAAACCTATTCAAGTCTGAGTTGAAAATTACATTCCCAGTATTGCATTAT  
TGAGGTATTTAAGAAGATTATTTAGAGAAAAATATTCTCATTTGATATAATTCTCTG  
TTCACTGTGAAAAAAAGAAGATATTCCATAAATGGGAAGTTGCCATTGTCTCAAG  
AAATGTGTTTCAAGTGCACATTCTGGTCTTTAGAGGTATATTCCAAATTCCCTTGT  
ATTTTAGGTTATGCAACTAAACACTACCTTACATTAATTACAGTTCTACACA  
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTAAGTTCATGGTATTCTCTTGATTC  
CAACAAAGTTGATTTCTCTGTATTTCTTACTTACTATGGTTACATTTTATT  
CAAATTGGATGATAATTCTGGAAACATTTTATGTTTAGAAACAGTATTGTTGTT  
GTTTCAAACTGAAGTTACTGAGAGATCCATCAAATTGAACAACTGTTGAATTAAATT  
TTGGCCACTTTTCAGATTTACATCATTCTGCTGAACCTCAACTGAAATTGTTTT  
TTTCTTTGGATGTAAGGTGAACATTCTGATTTGTCATGTGAAAAAGCCTGGTA  
TTTACATTGAAATTCAAAGAACGTTAATATAAAAGTTGCATTCTACTCAGGAAAAAG  
CATCTTCTGTATATGCTTAAATGTATTTGTCCTCATATAACAGAAAGTTCTAATTGAT  
TTACAGTCTGTAATGCTGATGTTAAAATAACATTATTTATATTGTTAAAAGACAA  
ACTTCATATTATCCTGTGTTCTTCTGACTGGTAATATTGTGTTGGGATTCACAGGTAAA  
GTCAGTAGGATGGAACATTAGTGTATTTACTCCTAAAGAGCTAGAATAACATAGTTT  
CACCTTAAAGAAGGGGGAAATCATAAAACAAATGAATCAACTGACCATTACGTAGTAGAC  
AATTCTGTAATGTCCTTCTTCTAGGCTCTGTTGCTGTGAATCCATTAGATTACAG  
TATCGTAATATAACAGTTCTTAAAGCCCTCCTTGAATTTAAATATTGTACCA  
AAAGAGTTGGATGTAATTGTGATGCCTTAGAAAATATCCTAAGCACAAATAACCT  
TTCTAACCACTTCATTAAGCTGAAAAAA

## **FIGURE 114**

MAPSGSLAVPLAVLVLLLWGPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL  
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI  
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL  
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPPSKLLSESAQPLKKVEEEQEADEEDVSE  
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 182-201

**Casein kinase II phosphorylation site.**

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

**Tyrosine kinase phosphorylation site.**

amino acids 107-115

**N-myristoylation site.**

amino acids 20-26, 192-198

**Amidation site.**

amino acids 25-29

## **FIGURE 115**

GCGAGTGTCCAGCTCGGGAGACCCGTGATAATTGTTAACTAATTCAACAAACGGGACCCCTT  
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCAGGATTGGAAGAGCGGG  
AAGGTCCCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC  
ATTGCTGATGGCTGGTTGGTGTCTGAGCTGTGAGGCGAATTCTCACCTCTATTG  
GGCACATGACTGACCTGATTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC  
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGGCCAACAAAATGGAAGCCTGAC  
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGG  
TGAAGCGGCTAACACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA  
GGTTTATGCCAACCTCTGTGAGCGGAGTTCTCCCCACTGATGAGGACGGAGATAGG  
AGCTGCCAACGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA  
GAGGGGAACCTCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG  
GGCGCTCGGCCTACAATGAAGGGGACTATTATCATACTGGTGTGTGGATGGAGCAGGTGCT  
AAAGCAGCTTGATGCCGGGGAGGAGGGCACCACAACCAAGTCACAGGTGCTGGACTACCTCA  
GCTATGCTGCTTCCAGTGGGTGATCTGCACCGTGCCCTGGAGCTCACCGCCGCTGCTC  
TCCCTGACCCAAGCCACGAACGAGCTGGAGGGAACTGCGGTACTTGAGCAGTTATTGGA  
GGAAGAGAGAGAAAAAACGTTAACAAATCAGACAGAACGCTGAGCTAGCAACCCCAGAAGGCA  
TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTACGAGAGCCTGTGCTGG  
GAGGGTGTCAAACGTACACCCGTAGACAGAACGAGGCTTCTGTAGGTACCAACATGGCAA  
CAGGGCCCCACAGCTGCTATTGCCCTTCAAAGAGGAGGACAGTGGACAGCCCGCACA  
TCGTCAGGTACTACGATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA  
CCTAAACTTGACGAGCCACCGTTGTGATCCAAGAACAGGAGTCTCACTGTGCCAGCTA  
CCGGGTTTCAAAGCTCCTGGCTAGAGGAAGATGATGACCTGTTGTGGCCCGAGTAAATC  
GTGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT  
TATGGAGTGGGAGGACAGTATGAACCGCACTCGACTTCTCTAGGCAGCCTTGTACAGCGG  
CCTCAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGAAGCTG  
GTGGTGCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTAAGAAGGGTACAGCTGTG  
TTCTGGTACAACCTCTGCGGAGCGGGGAAGGTGACTACCGAACAGACATGCTGCC  
TGTGCTTGTGGCTGCAAGTGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT  
TGAGACCTTGTGGATCAACAGAACGTTGACTGACATCCTTCTGTCTCCCTCCTGGTC  
CTTCAGCCCATGTCACAGTGCAGACACACCTTGTATGTTCTTGTATGTTCTATCAGGCT  
GATTTTGGAGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT  
GTGACTGAAGTCCCAGCCCTTCATTAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA  
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCCTTGTACCTCAGGTGTT  
TTAGGTGTGAGATGTTCACTGAACCAAAGTTCTGATACCTGTTACATGTTGTTTAT  
GGCATTCTATCTATTGTGGCTTACCAAAAAAATGTCCCTACCAGAAAAAA

## **FIGURE 116**

MKLWVSALLMAWFGVLSHVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA  
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP  
TDEDEIGAAKALMRLQDTYRLDPGTISRGELPGTKYQAMLSVDDCFGMGRSAYNEGDDYYHTV  
LWMEQVLKQLDAGEEATTKSQVLDYLSYAVFQLGDLHRAELTRRLSLDPSHERAGGNLR  
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPVDPYLPERDVYESLCRGEVKLTPRRQKRLF  
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYYDVMSEEEIERIKEIAKPKLARATVRDPKTG  
VLTVASYRVSKSSWLEEDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHDFDS  
RRPFDGKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKGTAVFWYNLLRSGEDYR  
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEVD

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 115-119, 264-268

**Glycosaminoglycan attachment site.**

amino acids 490-494

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

**Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534

**Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

**N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

**Leucine zipper pattern.**

amino acids 213-235

## FIGURE 117

GCAGTATTGAGTTTACTCCTCCTTTAGTGGAAAGACAGACCATATCCCAGTGTGAGTGAAATTGATTGT  
TTCATTTATTACCGTTTGGCTGGGGTTAGTTCGACACCTTCACAGTGAAGAGCAGGCAGAAGGAGTTGTGA  
AGACAGGACAATCTTCTGGGGATGCTGGTCTGGAAAGCCAGCGGGCCTGCTCTGCTTGGCCTCATTGACCC  
CAGGTCTCTGGTAAACACTGAAAGCCTACTACTGGCCTGGTCCCCATCAATCCATTGATCCTTGAGGCTGTGCC  
CCTGGGCACCCACCTGGCAGGGCTACCACCATGCGACTGAGCTCCCTGTTGGCTCTGCTGCGGCAGCGCTTC  
CCCTCATCTTAGGGCTGCTCTGGGGTGCAGCCTGAGCCTCTGGGGTTCTGGATCCAGGGGAGGGAGAAG  
ATCCCTGTGTCGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCCAGATTGAGAGCTCGGCTAGACCAAAGTG  
ATGAAGACTTCAAACCCCGATTGTCCTACTACAGGGACCCACAAGCCCTACAAGAAGGTGTCAGGACTC  
GGTACATCCAGACAGAGCTGGGCTCCGTGAGCGGTTGCTGGTGGCTGACCTCCGAGCTACACTGTCCA  
CTTGGCCGTGGCTGTGAACCGTACGGTGGCCATCACTTCCCTCGGTTACTCTACTTCAGTGGCAGCGGGGG  
CCCGGGCTCCAGCAGGGATGCGAGGTGGTGTCTCATGGGATGAGCGGCCGCTGGCTCATGTCAGAGACCCCTGC  
GCCACCTTACACACACTTGGGGCCGACTACGACTGGTTCTCATGCAAGGATGACACATATGTGCAGGCC  
CCCGCTGGCAGCCCTGCTGGCCACCTCAGCATCAACCAAGACCTGACTTAGGCCGGCAGAGGAGTTCATTG  
GCGCAGGCAGCAGGGCCGGTACTGTCACTGGGGCTTTGGTACCTGGTGTACGGAGTCTCTGCTTCGTC  
GGCCACATCTGGATGGCTGCCAGGGAGACATTCTCAGTGGCTGTGACGAGTGGCTGGACGCTGCCCTCATTG  
ACTCTCTGGCGTGGCTGTCTCACAGCACCAGGGCAGCAGTATGCTCATTTGAACACTGGCCAAAAATAGGG  
ACCTGAGAAGGAAGGGAGCTGGCTTCTGAGTGCCTTCGGCTGACCCCTGCTCTGGCAAGGTACCCCTATGT  
ACCGCTCCACAAACGCTTCAGCGCTCTGGAGTTGGAGCGGCTTACAGTAAATAGAACAACTGAGGCTCAGA  
TCCGGAACCTGACCGTGTGACCCCCGAAGGGGAGGAGGGCTGAGCTGGCCGTTGGCTCCCTGCTCCTTCA  
CACACACACTCTGCTTGGAGGTGCTGGCTGGACTACTTCACAGAGCAGCACACCTCTCTGTCAGATGGG  
CTCCAAGTGCCACTACAGGGGCTAGCAGGGCGACGGTGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA  
ATCGCGCTATCAGCCCCGCTGCGCTTCCAGAACGCGACTGCTCAACGGCTATCGGCCCTCGACCCAGCAC  
GGGGCATGGAGTACACCCCTGGACCTGCTTGGAAATGTTGACACAGCGTGGCACCGGGGGCCCTGGCTCGCA  
GGGTCAGCCTGCTGCCACTGAGCCGGTGGAAATCTACCTATGCCCTATGTCAGTGGCCACCCGAGTGC  
AGCTGGTGTGCCACTCTGGTGGCTGAAGCTGCTGAGCCCCGGTTCTGAGGCCAGGCTTGAGCCAATGTC  
TGGAGCCACGAGAACATGCTTGTGACCCCTGTTGCTGGTCTACGGGCCACGAGAACGGTGGCCGTGGAGCTCCAG  
ACCCATTCTGGGTGAAGGCTGAGCGAGGTTAGAGCAGGGTACCTGGACGAGGCTGGCTGGAGCTGGCTCG  
CTGTCGAGCAGAGGCCCTTCCCAGGTGCGACTCATGGACGTGGTCTGAAGAACGACCCCTGTGGACACTCT  
TCTTCTTACCAACCGTGTGGACAAGGCTGGCCGAAGTCTCAACCGCTGTCAGTGAATGCCATCTGGCT  
GGCAGGCCCTTCCAGTCATTCAGGAGTTCAATCTGCCCTGTCACACAGAGATCACCCCCAGGGCCCC  
CGGGGGCTGGCCCTGACCCCCCTCCCTGGTGTGACCCCTCCGGGGGCTCCATAGGGGGAGATTG  
ACCGCAGGCTCTGGAGGGCTGCTTCTACACGCTGACTACCTGGCGGCCGAGCCCGCTGGCAGGTGAAC  
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGGCTGGAGGTGATGGATTTCTCCCTGGAGACTGCA  
ACCTCTTCGGCCGTAGAGCCAGGGCTGGTGCAGAACGTTCTCCCTGGAGACTGCAAGCCACGGCTCA  
AACTCTACCAACCGCTGCCCTCAGAACCTGGAGGGCTAGGGGCCGTGCCAGCTGGCTATGGCTCTTTG  
AGCAGGAGCAGCCAATAGCACTAGCCGCTGGGGCCCTAACCTCATTACCTTGTCTGCCAGCC  
CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTAAATATGAAAATGTTATTAA  
ACATGTCTTGTGCC

## **FIGURE 118**

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD  
QSDEDFKPRIVPYYRDPNKPYKKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV  
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHFGADYDWFFIMQDDTY  
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLPHLDGCRG  
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE  
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPGEAGLSWPVGLPAPFTPNSRFEV  
LGWDYFTEQHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRYQPRLRFQKQRLLNGYR  
RFDPARGMEYTL DLL ECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVPL  
VAEAAAAPAFLEAFANVLEPREHALL TLL VYGPREGGRGAPDPFLGVKAAAELERRYPG  
TRLAWLAVRAEAPSQVRLMDVSKKHPVDTLFFLTTWTRPGPEVLNRCRMNAISGWQAFFP  
VHFQEFNPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA  
RARLAGELAGQEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR  
CRLSNLEGLGGRAQLAMALFEQEANST

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 489-507

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-678

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## **FIGURE 119**

CGGAGTGGTGCGCCAACGTGAGAGGAAACCGTGC CGGCTGC GCTT CCTGTCCCAGCC  
GTTCTAGACGCCGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTGATGCTGG  
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTATGGAAATAGAA  
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTGAAAATTCA  
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC  
CAAAGATGTGAGTCTTGGCTGCAGTAAAGGAGACTGGACAAACACTGTGACAAAGCAG  
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCAATTATGGACACAAATGACATG  
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACAAC  
GTTCTCCTGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA  
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT  
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTAACAGCCTCT  
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAAGATATCTGAAGATAAAC  
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGCAGAAAATGCAGAAGATGCTGATGGA  
AAAGATGTATTAATACAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC  
CAACCAGGTAGTAGAAGGCTGTTGTCAGATATGGCTTTACTTTAATGGACTGACTCAA  
ATCAGATGCATGTGATGTATGGGTATACCGCCTAGGGCATTGGCATATTTCAT  
GATGCATTGGTTCTTACCTCCAAATGGTCTGACAATGACTGAGAAGTGGTAGAAAAGCG  
TGAATATGATCTTGTATAGGACGTGTTGTCATTATTGTAGTAGTAACATACATATCAA  
TACAGCTGTATGTTCTTTCTTTCTAATTGGTGGCACTGGTATAACCACACATTAAAG  
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTTAAAACACATGAACATTGTAAATG  
TGTTGGAAAGAAGTGTGTTAAGAATAATAATTGCAAATAACTATTAATAAAATTATAT  
GTGATAAAATTCTAAATTATGAACATTAGAAATCTGTGGGCACATATTGCTGATTGGTT  
AAAAAAATTAAACAGGTCTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT  
TGTGATTAAAGTAAAACCTTCTAGCTGTGTTCCCTTACTCTAATACGTATTATGTTCT  
AAGCCTCCCCAAGTTCCAATGGATTGCTTCTCAAAATGTACAACTAAGCAACTAAAGAAA  
ATTAAAGTGAAAGTGTAAAAAT

## **FIGURE 120**

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME  
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKFESINMDTNMDWLMMRK  
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHТИKSGDLEYVGMEGG  
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT  
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL  
PPNGSDND

**Signal sequence:**

amino acids 1-33

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-672

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## **FIGURE 121**

CCACCGTCCGATCTTACCAACAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG  
AAAAAGAGAGAGAGAGAAACAAAAACCAAGAGAGAGAAAAATGAATTCATCTAAATCAT  
CTGAAACACAATGCACAGAGAGAGGATGCTCTCTCCAAATGTTCTTATGGACTGTTGCT  
GGGATCCCCATCCTATTCAGTGCCTGTTCATCACCAGATGTGTTGACATTCGCAT  
CTTCAACCTGTGATGAGAAAAGTTCAGCTACCTGAGAATTTCACAGAGCTCTGCT  
ACAATTATGGATCAGGTTCAGTCAGAATTGTTGTCATTGAACGGAAATTTCATCC  
AGCTGCTACTTCTTTCTACTGACACCATTCCCTGGCGTTAAGTTAAAGAACTGCTCAGC  
CATGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCTTCTACAAGA  
AACCTAAAATGAGAGAGTTTTTATTGGACTGTCAGACCAGGTTGTCGAGGGTCAGTGGCAA  
TGGGTGGACGGCACACCTTGACAAAGTCTCTGAGCTCTGGATGTAGGGAGCCAAACAA  
CATAGCTACCCCTGGAGGACTGTGCCACCATGAGAGACTCTCAAACCCAAGGCAAAATTGGA  
ATGATGTAACCTGTTCTCAATTATTCGGATTGTGAAATGGTAGGAATAATCCTTG  
AACAAAGGAAAATCTTTTAAGAACAGAACGGACAACCTCAAATGTGAAAGGAAGAGCA  
AGAACATGCCACACCCACCGCCCCACACGAGAAATTGTGCGCTGAACCTCAAAGGACTTC  
ATAAGTATTGTTACTCTGATACAAATAAAATAAGTAGTTAAATGTTAAAAAAAAAAAA  
AAA  
AAAAA

□ 500 500 500 500 500  
■ 100 100 100 100 100

## **FIGURE 122**

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN  
FTELSCNYGSGSVKNCCPLNWEYFQSSCYFFSTDТИWALSLKNCSAMGAHLVVINSQEEQ  
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNNIATLEDATMRDSS  
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

**Signal sequence:**

amino acids 1-42

**N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

**Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

**N-myristoylation site.**

amino acids 15-21, 74-80, 155-161

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38

## **FIGURE 123**

GGGACTACAAGCCGCGCCCGCTGCCGCTGGCCCCCTCAGCAACCCCTCGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCTGCTGCTGCTTTCAAGGGCTGCCTGATAGGGGCTGTAAATC  
TCAAATCCAGCAATCGAACCCCCAGTGGTACAGGAATTGAAAGTGTGGAACTGTCTTGCATCATTACGGATTGCG  
AGACAAGTGAACCCAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTGACAACAAAA  
TTCAGGGAGACTTGGCGGGCTGAGAAATACTGGGAAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG  
ACTCAGCCCTTATCGCTGTGAGGTCGTTGCTGAAATGACCGAAGGAAATTGATGAGATTGTGATCGAGTAA  
CTGTGCAAGTGAAGCCAGTGAACCCCTGTCTGAGAGTGGCGAAGGCTGTACCAAGTAGGCAAGATGGCAACACTGC  
ACTGCCAGGAGAGTGGAGGGCCACCCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT  
CCAGAGCCAATCCCAGATTGCAATTCTTCTTCACTTAAACTCTGAAACAGGCACTTGGTGGTCACTGCTG  
TTCACAAGGAGCAGTCTGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG  
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGTTCTGGTTGTCCTTGTACTGGCCCTGA  
TCACGTTGGGCATCTGCTGTGCATACAGACGGCTACTTCATCAACAATAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGAAACAGATGGAGTTAACATACATCCGCACTGACGAGGGCCACTTCAGACACAAGTCATGTTG  
TGATCTGAGACCCGCGGTGCGCTGAGAGCGCACAGAGCGCACGTGCACATACTCTGCTAGAAAACCTCTGTC  
GGCAGCGAGAGCTGACTCGGACAGAGCTAGACACTCATTAGAAGCTTTCAGGATGGACCCGGTAAATATAACCAA  
CTACTCTTACTCTAACAGGCCATGAATAGAAGAATTTCAGGATGGACCCGGTAAATATAACCAA  
GGAAGCGAAACTGGGTGGCTTCACTGAGTTGGGTTCTAATCTGTTCTGGCTGATTCCGCATGAGTTAGG  
GTGATCTTAAAGAGTTGCTCACGAAACGCCGTGCTGGGCCCTGTGAAGCCAGCATGTTCAACTGGTCGTT  
CAGCAGCCACGACAGCACCATGTGAGAGTGGCGAGGTGGTGGACAGCACCAGCAGCGCATCCGGGGAAACCA  
GAAAAGGCTTCTACACAGCAGCCTTACTTCATGGCCACAGACACCACCGCAGTTCTTAAAGGCTCTGC  
TGATCGGTGTTGCACTGTCATTGGAGAAGCTTTGGATCAGCATTTGTAACAAACAAATCAGGAAG  
GTAAATTGGTTGCTGGAAGAGGGATCTTGCCTGAGGAACCCCTGTTGCTTCAACAGGGTGTCAAGGATTTAAGGAA  
ACCTTCGCTTAAAGCTAAGTCTGAAATGGTACTGAAATATGCTTTCTATGGGCTTGTGTTATTAAACCA  
TACATCTAAATTGGCTAACGGATGTATTGATTATTGAAAAGAAAATTCTATTTAAACTGTAATATATTGT  
CATACATGTTAAATAACCTATTTTAAAGGTTAACCTAACGGTAGAAGTCAAGCTACTAGTGTAAAT  
TGGAAAATATCAATAATTAGAGTATTGACAGGAACTCTCATGGAAAGTTACTGTGATGTTCTTCT  
CACACAAGTTTACGCTTTTCAAAAGGAACCTACACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAATTCCAGTTAACGAAATGTTGAAATCAGTTGCTCTCTTCAAAAGAAACCTCTCAGGTTAGCTTGA  
GCCTCTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCTCAGATGTACATACAGATG  
CCAGTCAGCTCTGGGTGCGCCAGGCCAGCGCTAGCTCACTGTCCTCGCTGCTGCCAGGAGGCC  
GCCATCCTGGCCCTGGCAGTGGCTGTGCTCCAGTGAGCTTACTCAGTGCCCTTGCTCATCCAGCACAGC  
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGCTAGCGTCCCAGCTTGGCTCTGTAA  
TTTGTTATGGATGGCTCACAAAATAGGGCCCCAATGCTATTGTTAAAGTTGTTAATTATTGTT  
AAGATTGCTAACGGCAAAGGCAATTGGAAATCAACTGTCAAGTACAATAACATTAAAAGAAAATGGAT  
CCCACGTGTTCTTGCACAGAAGAACCCAGGCCACAGGCTCTGTCGCAATTCAAAACAAACCATGAT  
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAAGGTGGAGCAGCCAGGTGAAAGGCTGGCGGGAGGAAAG  
TGAAAAGCCTGAATCAAAGCAGTTCTAACATTGACTTTCAATTGACTTTCACTCCGAGACACTGCT  
TGTGGGGGACATTGCAACATCACTCAGAACCTGTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCC  
GCCGTGCTGGACTCAGGACTGAAGTGTGTAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGCT  
GAATGGCTCTCAACTCACCTGCTTTCAGCTTCACTGCTTGGGTTTTTAACTTGCACAGCTTTTT  
AATTGCAACATGAGACTGTGTTGACTTTTTAGTTATGTGAAACACTTGCAGGCCCTGGCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTGCTGCATGGCATTCTGGATGCTTAGCATGCAAGT  
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCCCTCAGCGTTGGGATTACGCTCCAGCCT  
TCTTGGTTGTCAGTGATAGGGTAGCCTTATTGCCCCCTTCTTAACTCTAAACCTTCTACACTAGTGCA  
TGGGAACCAAGTCTGAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA  
CGGAAAAGGAATACTCGTGTTAGATGAATGTGACTCAAGACTCGAGGCCGATAACGGGCTGTGATTCT  
GCCTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTGGCATTGTTAAC  
CTCATTATAAAAGCTTCAAAAAACCA

## **FIGURE 124**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFLLLLFRGCLIGAVNLKSSNRTPVVQEFESELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSKIKWNVRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267